

SEQUENCE LISTING

<110> Renner, Wolfgang A.
Bachmann, Martin
Tissot, Alain
Maurer, Patrick
Lechner, Franziska
Sebbel, Peter
Piossek, Christine

<120> Molecular Antigen Array

<130> 1700.0190004

<140> (To be assigned)
<141> 2002-01-18

<150> US 60/262,379
<151> 2001-01-19

<150> US 60/288,549
<151> 2001-05-04

<150> US 60/326,998
<151> 2001-10-05

<150> US 60/331,045
<151> 2001-11-07

<160> 350

<170> PatentIn Ver. 2.1

<210> 1
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 1
ggggacgcgt gcagcaggta accaccgtta aagaaggcac c

41

<210> 2
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 2
cggtggttac ctgctgcacg cggtgcttaa gcgacatgta gcgg

44

<210> 3
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 3
ccatgaggcc tacgataccc 20

<210> 4
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Primer

<400> 4
ggcaactcacg ggcgcgttta caggc 25

<210> 5
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 5
ccttcattaa cggtggttac ctgctggcaa ccaacgtgg tcatgac 47

<210> 6
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6
aagcatgctg cacgcgtgtg cggtggtcgg atcggccggc 40

<210> 7
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
gggtctagat tcccaaccat tcccttatcc aggcttttg acaacgctat gctccgcgcc 60
catcgctgc accagctggc ctttgacacc 90

<210> 8
<211> 108
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
gggtctagaa ggaggtaaaa aacgatgaaa aagacagcta tcgcgattgc agtggcactg 60
gctggtttcg ctaccgtagc gcaggccttc ccaaccattc ccttatcc 108

<210> 9
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
cccgaaattcc tagaagccac agctgccctc c 31

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
cctgcgggtgg tctgaccgac accc 24

<210> 11
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
ccgcggaaga gccaccgcaa ccaccgtgtg ccgccaggat g 41

<210> 12
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
ctatcatcta gaatgaatag aggattcttt aac 33

<210> 13
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified ribosome
binding site

<400> 13
aggaggtaaa aaacg 15

<210> 14
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: signal peptide

<400> 14
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1 5 10 15
Thr Val Ala Gln Ala
20

<210> 15
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified Fos
construct

<400> 15
Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu
1 5 10 15
Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu
20 25 30
Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
35 40 45

<210> 16
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide linker

<400> 16
Ala Ala Ala Ser Gly Gly
1 5

<210> 17
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide linker

<400> 17
Gly Gly Ser Ala Ala Ala

1 5

<210> 18
<211> 256
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion construct

<400> 18
gaattcagga ggtaaaaaac gatgaaaaag acagctatcg cgattgcagt ggcactggct 60
ggtttcgcta ccgtagcga ggcctgggtg gggcggccg cttctgggtt ttgcgggtgg 120
ctgaccgaca ccctgcaggc gaaaccgac caggtggaaag acgaaaaatc cgcgctgcaa 180
accgaaatcg cgaacctgct gaaagaaaaa gaaaagctgg agttcatcct ggcggcacac 240
ggtggttgc aagtt 256

<210> 19
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion construct

<400> 19
Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
5 10 15
Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
20 25 30
Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
35 40 45

His Gly Gly Cys
50

<210> 20
<211> 261
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<220>
<221> CDS
<222> (22) .. (240)

<400> 20
gaattcagga ggtaaaaaac g atg aaa aag aca gct atc gcg att gca gtg 51
Met Lys Lys Thr Ala Ile Ala Ile Ala Val
1 5 10
gca ctg gct ggt ttc gct acc gta gcg cag gcc tgc ggt ggt ctg acc 99
Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Cys Gly Gly Leu Thr
15 20 25

gac acc ctg cag gcg gaa acc gac cag gtg gaa gac gaa aaa tcc gcg	147	
Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala		
30	35	40
ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag ctg gag	195	
Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu		
45	50	55
ttc atc ctg gcg gca cac ggt ggt tgc ggt ggt tct gcg gcc gct	240	
Phe Ile Leu Ala Ala His Gly Gly Cys Gly Ser Ala Ala Ala		
60	65	70
gggtgtgggg atatcaagct t	261	

<210> 21
<211> 73
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion construct

<400> 21
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1 5 10 15

Thr Val Ala Gln Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu
20 25 30

Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala
35 40 45

Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His
50 55 60

Gly Gly Cys Gly Ser Ala Ala Ala
65 70

<210> 22
<211> 196
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion construct

<220>
<221> CDS
<222> (34) .. (189)

<400> 22
gaattcagga ggtaaaaaga tatcgggtgt ggg gcg gcc gct tct ggt tgc 54
Ala Ala Ala Ser Gly Gly Cys
1 5

ggt ggt ctg acc gac acc ctg cag gcg gaa acc gac cag gtg gaa gac 102
Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp
10 15 20

gaa aaa tcc gcg ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa 150
Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys
25 30 35

gaa aag ctg gag ttc atc ctg gcg gca cac ggt ggt tgc taagctt 196
Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
40 45 50

<210> 23
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<400> 23
Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
1 5 10 15
Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
20 25 30
Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
35 40 45
His Gly Gly Cys
50

<210> 24
<211> 204
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<400> 24
gaattcagga ggtaaaaaac gatggcttgc ggtggctctga ccgacacccct gcaggcgaa 60
accgaccagg tggaaagacga aaaatcccgctg cttccaaaccg aaatcgcaaa cctgctgaaa 120
gaaaaagaaa agctggagtt cttccctggcg gcacacgggtg gttgcgggtgg ttctgcggcc 180
gctgggtgtg gggatataa gctt 204

<210> 25
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<400> 25
Lys Thr Met Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr
1 5 10 15
Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn

20 25 30
Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly
35 40 45
Gly Cys Gly Gly Ser Ala Ala Ala
50 55

<210> 26
<211> 26
<212> PRT
<213> Homo sapiens

<400> 26
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Ala Phe Gly Leu Leu
1 5 10 15
Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala
20 25

<210> 27
<211> 262
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<400> 27
gaattcaggc ctatggctac aggctcccg agtccctgc tcctggcttt tggcctgctc 60
tgcctgcctt ggcttcaaga gggcagcgct gggtgtgggg cggccgcctc tggtggttgc 120
ggtggtctga ccgacaccct gcaggcgaa accgaccagg tggaaagacga aaaaatcccg 180
ctgcaaaccg aaatcgcgaa cctgctgaaa gaaaaagaaa agctggagtt catcctggcg 240
gcacacgggtt gttgctaagc tt 262

<210> 28
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<400> 28
Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
5 10 15

Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
20 25 30

Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
35 40 45

His Gly Gly Cys
50

<210> 29

<211> 261
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<220>
<221> CDS
<222> (7)...(240)

<400> 29
gaattc atg gct aca ggc tcc cgg acg tcc ctg ctc ctg gct ttt ggc 48
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly
1 5 10
ctg ctc tgc ctg ccc tgg ctt caa gag ggc agc gct tgc ggt ggt ctg 96
Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Cys Gly Gly Leu
15 20 25 30
acc gac acc ctg cag gcg gaa acc gac cag gtg gaa gac gaa aaa tcc 144
Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser
35 40 45
gcg ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag ctg 192
Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu
50 55 60
gag ttc atc ctg gcg gca cac ggt ggt tgc ggt ggt tct tct gcg gcc gct 240
Glu Phe Ile Leu Ala Ala His Gly Gly Cys Gly Ser Ala Ala Ala
65 70 75
gggtgtggga ggcctaagct t 261

<210> 30
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<400> 30
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15
Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Cys Gly Gly Leu Thr Asp
20 25 30
Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu
35 40 45
Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
50 55 60
Ile Leu Ala Ala His Gly Gly Cys Gly Ser Ala Ala Ala
65 70 75

<210> 31
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
cctgggtggg ggccggccgct tctgggtggtt gcgggtggct gacc

44

<210> 32
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
ggtgggaatt caggaggtaa aaagatatcg ggtgtggggc ggcc

44

<210> 33
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
ggtgggaatt caggaggtaa aaaacgtatgg cttgcggatgg tctgacc

47

<210> 34
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 34
gcttgcggtg gtctgacc

18

<210> 35
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
ccaccaagct tagcaaccac cgtgtgc

27

<210> 36
<211> 54
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 36

ccaccaagct tgatatcccc acacccagcg gccgcagaac caccgcaacc accg

54

<210> 37

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 37

ccaccaagct taggcctccc acacccagcg gc

32

<210> 38

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 38

ggtgggaatt caggaggtaa aaaacgatg

29

<210> 39

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 39

gttgggaatt caggcctatg gctacaggct cc

32

<210> 40

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 40

gttgggaatt catggctaca ggctccc

27

<210> 41

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 41
gggtctagaa tggctacagg ctcccgacg tccctgctcc tggctttgg cctgctctg 59

<210> 42
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 42
cgcaggcctc ggcactgccc tcttgaagcc agggcaggca gagcaggcca aaagccag 58

<210> 43
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified bee
venom phospholipase A2

<220>
<221> CDS
<222> (1)...(402)

<400> 43
atc atc tac cca ggt act ctg tgg tgt ggt cac ggc aac aaa tct tct 48
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
1 5 10 15

ggc ccg aac gaa ctc ggc cgc ttt aaa cac acc gac gca tgc tgt cgc 96
Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
20 25 30

acc cag gac atg tgt ccg gac gtc atg tct gct ggt gaa tct aaa cac 144
Thr Gln Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
35 40 45

ggg tta act aac acc gct tct cac acg cgt ctc agc tgc gac tgc gac 192
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
50 55 60

gac aaa ttc tac gac tgc ctt aag aac tcc gcc gat acc atc tct tct 240
Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser
65 70 75 80

tac ttc gtt ggt aaa atg tat ttc aac ctg atc gat acc aaa tgt tac 288
Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
85 90 95

aaa ctg gaa cac ccg gta acc ggc tgc ggc gaa cgt acc gaa ggt cgc 336
Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
100 105 110

tgc ctg cac tac acc gtt gac aaa tct aaa ccg aaa gtt tac cag tgg 384
Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
115 120 125

ttc gac ctg cgc aaa tac 402
Phe Asp Leu Arg Lys Tyr
130

<210> 44
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified bee
venom phospholipase A2

<400> 44
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser 15
1 5 10 15
Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg 30
20 25 30
Thr Gln Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His 45
35 40 45
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp 60
50 55 60
Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser 80
65 70 75 80
Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr 95
85 90 95
Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg 110
100 105 110
Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp 125
115 120 125
Phe Asp Leu Arg Lys Tyr
130

<210> 45
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 45 19
ccatcatcta cccaggtac

<210> 46
<211> 34
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 46
cccacaccca gcggccgcgt atttgcgcag gtcg 34

<210> 47
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 47
cggtggttct gcggccgcta tcatctaccc aggtac 36

<210> 48
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 48
ttagtatttg cgcaaggatcg 19

<210> 49
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 49
ccggctccat cggtgcag 18

<210> 50
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 50
accaccagaa gcggccgcag gggaaacaca tctgcc 36

<210> 51
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 51

cggtggttct gcggccgctg gctccatcg	35
<210> 52	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Primer	
<400> 52	
ttaaggggaa acacatctgc c	21
<210> 53	
<211> 33	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Primer	
<400> 53	
actagtctag aatgagagtg aaggagaaaat atc	33
<210> 54	
<211> 42	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Primer	
<400> 54	
tagcatgcta gcaccgaatt tatctaattc caataattct tg	42
<210> 55	
<211> 51	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Primer	
<400> 55	
gtagcaccca ccaaggcaaa gctgaaagct acccagctcg agaaaactggc a	51
<210> 56	
<211> 48	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Primer	
<400> 56	
caaagctcct attcccaactg ccagtttctc gagctggta gctttcag	48

<210> 57
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 57
ttcggtgcta gcgggtggctg cggtggtctg accgac 36

<210> 58
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 58
gatgctgggc ccttaaccgc aaccaccgtg tgccgcc 37

<210> 59
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: JUN amino acid sequence

<400> 59
Cys Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys
1 5 10 15

Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln
20 25 30

Val Ala Gln Leu Lys Gln Lys Val Met Asn His Val Gly Cys
35 40 45

<210> 60
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FOS amino acid sequence

<400> 60
Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu
1 5 10 15

Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu
20 25 30

Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
35 40 45

<210> 61
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 61
ccggaaattca tgtgcgggtgg tcggatcgcc cg 33

<210> 62
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 62
gtcgctaccc gcggctccgc aaccaacgtg gttcatgac 39

<210> 63
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 63
gttggttgcg gagccgcgg tagcgacatt gaccctata aagaatttgg 50

<210> 64
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 64
cgcgtcccaa gcttctacgg aagcggtgat aggatagg 38

<210> 65
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 65
ctagccgcgg gttgcgggtgg tcggatcgcc cg 33

<210> 66
<211> 38
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 66
cgcgccccaa gcttttagca accaacgtgg ttcatgac 38

<210> 67
<211> 31
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 67
ccggattca tggacattga cccttataaa g 31

<210> 68
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 68
ccgaccaccc caacccgcgg ctagcgaaag cgttgatagg atagg 45

<210> 69
<211> 47
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 69
ctaattggatc cggggggggc tgcgggtggtc ggatcgcccg gctcgag 47

<210> 70
<211> 39
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 70
gtcgctaccc gcggctccgc aaccaacgtg gttcatgac 39

<210> 71
<211> 31
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 71
ccggaattca tggacattga cccttataaa g 31

<210> 72
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 72
ccgaccaccc cagcccccac cgatccatt agtacccacc caggtac 48

<210> 73
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 73
gttggttgcg gagccgcgg tagcgaccta gtagtcagtt atgtc 45

<210> 74
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 74
cgcgccccaa gcttctacgg aagcggtgat aggatagg 38

<210> 75
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 75
ctagccgcgg gttgcgggtgg tcggatcgcc cg 33

<210> 76
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 76

ACGATTCGTTGCGGCGT

cgcgtcccaa gcttttagca accaacgtgg ttcatgac	38
<210> 77	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Primer	
<400> 77	
ccggattca tggccacact tttaaggagc	30
<210> 78	
<211> 38	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Primer	
<400> 78	
cgcgtcccaa gcttttagca accaacgtgg ttcatgac	38
<210> 79	
<211> 31	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Primer	
<400> 79	
ccggattca tggacattga cccttataaa g	31
<210> 80	
<211> 51	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Primer	
<400> 80	
ccttagagcca cctttgccac catcttctaa attagtaccc acccaggtag c	51
<210> 81	
<211> 48	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Primer	
<400> 81	
gaagatggtg gcaaagggtgg ctctagggac ctagtagtca gttatgtc	48

<210> 82
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 82
cgcgccccaa gcttctaaac aacagtagtc tccggaag

38

<210> 83
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 83
gccgaattcc tagcagctag caccgaattt atctaa

36

<210> 84
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 84
gtttaagtgc acatgagagt gaaggagaaa tat

33

<210> 85
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 85
taaccgaatt caggaggtaa aaagatatgg

30

<210> 86
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 86
gaagtaaagc tttaaccac cgcaaccacc agaag

35

<210> 87
<211> 33
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 87

tcgaatgggc cctcatcttc gtgtgctagt cag

33

<210> 88

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fos fusion construct

<400> 88

Glu Phe Arg Arg
1

<210> 89

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 89

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Gly Ser Gln Cys

180

<210> 90
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 90
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60
Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr
65 70 75 80
Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110
Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125
Pro Pro Ala Tyr Arg Pro Thr Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140
Glu Thr Cys Val Ile Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160
Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175
Gln Ser Arg Gly Ser Gln Cys
180

<210> 91
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 91
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 92

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 92

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Asn Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 93

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 93

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Thr Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 94

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 94
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 95
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 95
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 96
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 96
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro Gln
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 97
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 97
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Lys Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Gly Ser Gln Cys
210

<210> 98
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 98
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30
Thr Ala Ser Ala Leu Phe Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60
Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ala
65 70 75 80
Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110
Asp Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125
Pro Pro Ala Tyr Arg Pro Ser Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140
Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160
Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175
Gln Ser Arg Glu Ser Gln Cys
180

<210> 99
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 99
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 100

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 100

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg His Ala Ile Leu Cys Trp Gly Asp Leu Arg Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 101
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 101
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Phe Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Ala Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Gln Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Cys
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 102
<211> 183
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
human Hepatitis B construct

<400> 102

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 103

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 103

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Ser
85 90 95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 104
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 104
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30
Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60
Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80
Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110
Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140
Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 105

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 105

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 106

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 106

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys

35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Ala Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Thr Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 107
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 107
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 108
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 108
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 109
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 109
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Thr Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ala Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 110
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 110
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Phe Glu Cys Ser Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 111
<211> 212
<212> PRT
<213> Hepatitis B virus

<220>
<221> UNSURE
<222> (28)
<223> May be any amino acid.

<400> 111
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Xaa Asp Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Ile Thr
85 90 95

Leu Ser Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Thr Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 112
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 112
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp Asn Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 113

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 113

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Cys Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 114

<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 114
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Pro Gln Cys
210

<210> 115
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 115
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Ser Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 116
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 116
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Leu Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 117
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 117
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Lys Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 118
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 118
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ala
50 55 60
Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 119
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 119
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Met Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Tyr Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Thr Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Gln Asp Pro Thr
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Val Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Val Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Gln Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 120

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 120

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg His Val Phe Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 121

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 121

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Thr Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 122

<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 122
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Ile Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 123
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 123
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Val
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Ala Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 124
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 124
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Asn
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp
100 105 110

Leu Val Val Gly Tyr Val Asn Thr Thr Val Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 125

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 125

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Thr Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 126

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 126

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr

1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Ala Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Ile Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 127
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 127
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Thr Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 128

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 128

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Arg Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Thr Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 129

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 129

Met Gln Leu Phe His Leu Cys Leu Val Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ala
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 130

<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 130
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Ala Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 131
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 131
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30
Thr Ala Ala Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 132

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 132

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Gly Ser Gln Cys
180

<210> 133
<211> 3221
<212> DNA
<213> Hepatitis B virus

<220>
<221> CDS
<222> (1901)..(2458)

<400> 133
ttccactgcc ttccaccaag ctctgcagga cccagagtc aggggtctgt atttcctgc 60
tggtggtcc agttcagggaa cagtaaaccc tgctccgaat attgcctctc acatctcg 120
aatctccgcg aggactgggg accctgtgac gaacatggag aacatcacat caggattc 180
aggaccctg ctcgtgttac aggccgggtt tttattgtt acaagaatcc tcacaatacc 240
gcagagtcta gactcgtggt ggacttctt caatttata gggggatcac ccgtgtgtct 300
tggccaaaat tcgcagtccc caacctccaa tcactcacca acctcctgtc ctccaattt 360
tcctggttat cgctggatgt gtctgcggcg tttatcata ttcctttca tcctgctgct 420
atgcctcattc ttcttattgg ttcttcttga ttatcaaggt atgttgcggg tttgtcctct 480
aattccagga tcaacaacaa ccagtaacggg accatgcaaa acctgcacga ctccgtctca 540
aggcaactct atgtttccct catgttgctg tacaaaacct acggttggaa attgcacctg 600
tattccatc ccacatgtcct gggcttcgc aaaataccta tgggagtggg cctcagtcgg 660
tttctttgg ctcagtttac tagtgcatt tggcatttgc ttcgtaggc tttccccac 720
tggggcatt tcagctatgtt ggtatgttgc gtattgggg ccaagtctgt acagcatcgt 780
gagtcctt ataccgtgt taccaatttt ctttgcgtc tgggtataca tttaaacccct 840
aacaacaaacaa aaagatgggg ttattcccta aacttcattgg gttacataat tggaaatgg 900
ggaacattgc cacaggatca tattgtacaa aagatcaaac actgttttag aaaacttcct 960
gttaacaggc ctattgattt gaaagtatgtt caaagaatttgc tgggtctttt gggctttgc 1020
gctccattta cacaatgtgg atatcctgcc ttaatgcctt tgcgtatgc tatacaggct 1080
aaacaggctt tcactttctc gccaacttac aaggccttgc taagtaaaca gtacatgaac 1140
ctttaccccg ttgctcggca acggccttgc ctgtgcggaa tttttgcgtc cgcaacccccc 1200
actggttggg gcttggccat aggccatcag cgcatgatgtt gaaaccttgc ggctcctctg 1260
ccgatccata ctgcggaaact cctagccgtc tttttgcgtc gcagccggc tggagcaag 1320
ctcatcgaa ctgacaattc tgcgtcctc tcgcggaaat atacatcggtt tccatggctg 1380

ctaggctgta ctgccaactg gatccttcgc gggacgtcct ttgtttacgt cccgtcggcg 1440
ctgaatcccg cggacgaccc ctctcgggc cgcttggac tctatcgcc ccttctccgt 1500
ctgccgttcc agccgaccac ggggcgcacc tctcttacg cggtctcccc gtctgtgcct 1560
tctcatctgc cggtccgtgt gcacttcgct tcacctctgc acgttgcatt gagaccaccg 1620
tgaacgccc tcaagatcctg cccaaggct tacataagag gactcttggaa ctcccaagcaa 1680
tgtcaacgac cgacccctgag gcctacttca aagactgtgt gtttaaggac tgggaggagc 1740
tgggggagga gattaggta aaggtcttg tattaggagg ctgttaggcat aaattggct 1800
gcgcaccaggc accatgcaac ttttcaccc ctgcctaattt atctcttgcataatgcccac 1860
tgttcaagcc tccaaagctgt gccttgggtg gcttggggc atg gac att gac cct 1915
Met Asp Ile Asp Pro
1 5
tat aaa gaa ttt gga gct act gtg gag tta ctc tcg ttt ttg cct tct 1963
Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro Ser
10 15 20
gac ttc ttt cct tcc gtc aga gat ctc cta gac acc gcc tca gct ctg 2011
Asp Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu
25 30 35
tat cga gaa gcc tta gag tct cct gag cat tgc tca cct cac cat act 2059
Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr
40 45 50
gca ctc agg caa gcc att ctc tgc tgg ggg gaa ttg atg act cta gct 2107
Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu Ala
55 60 65
acc tgg gtg ggt aat aat ttg gaa gat cca gca tcc agg gat cta gta 2155
Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu Val
70 75 80 85
gtc aat tat gtt aat act aac atg ggt tta aag atc agg caa cta ttg 2203
Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln Leu Leu
90 95 100
tgg ttt cat ata tct tgc ctt act ttt gga aga gag act gta ctt gaa 2251
Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Leu Glu
105 110 115
tat ttg gtc tct ttc gga gtg tgg att cgc act cct cca gcc tat aga 2299
Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg
120 125 130
cca cca aat gcc cct atc tta tca aca ctt ccg gaa act act gtt gtt 2347
Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val Val
135 140 145
aga cga cgg gac cga ggc agg tcc cct aga aga aga act ccc tcg cct 2395
Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
150 155 160 165
cgc aga cgc aga tct caa tcg ccg cgt cgc aga aga tct caa tct cgg 2443
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
170 175 180

gaa tct caa tgt tag tattccttgg actcataagg tggaaactt tactgggctt 2498
Glu Ser Gln Cys
185

tattcctcta cagtagctat cttaatcct gaatggcaaa ctccttcctt tcctaagatt 2558
catttacaag aggacattat tgataggtgt caacaatttg tggccctct cactgtaaat 2618
gaaaagagaa gattgaaatt aattatgcct gctagattct atcctaccca cactaaatat 2678

ttgcccttag acaaaggaat taaaccttat tatccagatc aggtagttaa tcattacttc 2738
caaaccagac attatttaca tactcttgg aaggctggta ttctatataa gaggaaacc 2798

acacgttagcg catcatttg cgggtcacca tattcttggg aacaagagct acagcatggg 2858

aggttggtca ttaaaacctc gcaaaggcat gggacgaat ctttctgttc ccaaccctct 2918

gggattctt cccgatcatc agttggaccc tgcattcgga gccaactcaa acaatccaga 2978

ttgggacttc aaccccatca aggaccactg gccagcagcc aaccaggtag gagtgggagc 3038

attcgggcca gggctcaccc ctccacacgg cggtatatttg gggtgagcc ctcaggctca 3098

ggcatattg accacagtgt caacaattcc tcctcctgcc tccaccaatc ggcagtcagg 3158

aaggcagcct actcccatct ctccacctct aagagacagt catcctcagg ccatgcagtg 3218

gaa 3221

<210> 134
<211> 185
<212> PRT
<213> Hepatitis B virus

<400> 134
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15
Ser Phe Leu Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60
Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala
65 70 75 80
Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95
Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140
Glu Thr Thr Val Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg
145 150 155 160
Arg Thr Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg
165 170 175
Arg Ser Gln Ser Arg Glu Ser Gln Cys
180 185

<210> 135
<211> 188
<212> PRT
<213> Woodchuck hepatitis B virus

<400> 135
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Leu
1 5 10 15

Asn Phe Leu Pro Leu Asp Phe Pro Asp Leu Asn Ala Leu Val Asp
20 25 30

Thr Ala Thr Ala Leu Tyr Glu Glu Leu Thr Gly Arg Glu His Cys
35 40 45

Ser Pro His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Asp Glu
50 55 60

Leu Thr Lys Leu Ile Ala Trp Met Ser Ser Asn Ile Thr Ser Glu Gln
65 70 75 80

Val Arg Thr Ile Ile Val Asn His Val Asn Asp Thr Trp Gly Leu Lys
85 90 95

Val Arg Gln Ser Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln
100 105 110

His Thr Val Gln Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Ala Pro Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu His Thr Val Ile Arg Arg Arg Gly Gly Ala Arg Ala Ser Arg Ser
145 150 155 160

Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro
165 170 175

Arg Arg Arg Arg Ser Gln Ser Pro Ser Thr Asn Cys
180 185

<210> 136
<211> 217
<212> PRT
<213> Ground squirrel hepatitis virus

<400> 136
Met Tyr Leu Phe His Leu Cys Leu Val Phe Ala Cys Val Pro Cys Pro
1 5 10 15

Thr Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp
20 25 30

Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Leu Asn Phe
35 40 45

Leu Pro Leu Asp Phe Pro Asp Leu Asn Ala Leu Val Asp Thr Ala
50 55 60

Ala Ala Leu Tyr Glu Glu Leu Thr Gly Arg Glu His Cys Ser Pro
65 70 75 80

His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Glu Glu Leu Thr
85 90 95

Arg Leu Ile Thr Trp Met Ser Glu Asn Thr Thr Glu Glu Val Arg Arg
100 105 110

Ile Ile Val Asp His Val Asn Asn Thr Trp Gly Leu Lys Val Arg Gln
115 120 125

Thr Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln His Thr Val
130 135 140

Gln Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Ala Pro
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu His Thr
165 170 175

Val Ile Arg Arg Arg Gly Gly Ser Arg Ala Ala Arg Ser Pro Arg Arg
180 185 190

Arg Thr Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg
195 200 205

Arg Ser Gln Ser Pro Ala Ser Asn Cys
210 215

<210> 137
<211> 262
<212> PRT
<213> Snow Goose Hepatitis B Virus

<400> 137

Met Asp Val Asn Ala Ser Arg Ala Leu Ala Asn Val Tyr Asp Leu Pro
1 5 10 15

Asp Asp Phe Phe Pro Lys Ile Glu Asp Leu Val Arg Asp Ala Lys Asp
20 25 30

Ala Leu Glu Pro Tyr Trp Lys Ser Asp Ser Ile Lys Lys His Val Leu
35 40 45

Ile Ala Thr His Phe Val Asp Leu Ile Glu Asp Phe Trp Gln Thr Thr
50 55 60

Gln Gly Met His Glu Ile Ala Glu Ala Ile Arg Ala Val Ile Pro Pro
65 70 75 80

Thr Thr Ala Pro Val Pro Ser Gly Tyr Leu Ile Gln His Asp Glu Ala
85 90 95

Glu Glu Ile Pro Leu Gly Asp Leu Phe Lys Glu Gln Glu Glu Arg Ile
100 105 110

Val Ser Phe Gln Pro Asp Tyr Pro Ile Thr Ala Arg Ile His Ala His
115 120 125

Leu Lys Ala Tyr Ala Lys Ile Asn Glu Glu Ser Leu Asp Arg Ala Arg
130 135 140

Arg Leu Leu Trp Trp His Tyr Asn Cys Leu Leu Trp Gly Glu Ala Thr
145 150 155 160

Val Thr Asn Tyr Ile Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu
165 170 175

Lys Tyr Arg Gly Arg Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro
180 185 190

Ile Gln Val Ala Gln Gly Gly Arg Lys Thr Ser Thr Ala Thr Arg Lys
195 200 205

Pro Arg Gly Leu Glu Pro Arg Arg Arg Lys Val Lys Thr Thr Val Val
210 215 220

Tyr Gly Arg Arg Arg Ser Lys Ser Arg Glu Arg Arg Ala Ser Ser Pro
225 230 235 240

Gln Arg Ala Gly Ser Pro Leu Pro Arg Ser Ser Ser Ser His His Arg
245 250 255

Ser Pro Ser Pro Arg Lys
260

<210> 138
<211> 305
<212> PRT
<213> Duck hepatitis B virus

<400> 138

Met Trp Asp Leu Arg Leu His Pro Ser Pro Phe Gly Ala Ala Cys Gln
1 5 10 15

Gly Ile Phe Thr Ser Ser Leu Leu Leu Phe Leu Val Thr Val Pro Leu
20 25 30

Val Cys Thr Ile Val Tyr Asp Ser Cys Leu Cys Met Asp Ile Asn Ala
35 40 45

Ser Arg Ala Leu Ala Asn Val Tyr Asp Leu Pro Asp Asp Phe Phe Pro
50 55 60

Lys Ile Asp Asp Leu Val Arg Asp Ala Lys Asp Ala Leu Glu Pro Tyr
65 70 75 80

Trp Arg Asn Asp Ser Ile Lys Lys His Val Leu Ile Ala Thr His Phe
85 90 95

Val Asp Leu Ile Glu Asp Phe Trp Gln Thr Thr Gln Gly Met His Glu
100 105 110

Ile Ala Glu Ala Leu Arg Ala Ile Ile Pro Ala Thr Thr Ala Pro Val
115 120 125

Pro Gln Gly Phe Leu Val Gln His Glu Glu Ala Glu Glu Ile Pro Leu
130 135 140

Gly Glu Leu Phe Arg Tyr Gln Glu Glu Arg Leu Thr Asn Phe Gln Pro
145 150 155 160

Asp Tyr Pro Val Thr Ala Arg Ile His Ala His Leu Lys Ala Tyr Ala
165 170 175

Lys Ile Asn Glu Glu Ser Leu Asp Arg Ala Arg Arg Leu Leu Trp Trp
180 185 190

His Tyr Asn Cys Leu Leu Trp Gly Glu Pro Asn Val Thr Asn Tyr Ile
195 200 205

Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu Lys Tyr Arg Gly Lys
210 215 220

Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro Ile Gln Val Ala Gln
225 230 235 240

Gly Gly Arg Asn Lys Thr Gln Gly Val Arg Lys Ser Arg Gly Leu Glu
245 250 255

Pro Arg Arg Arg Val Lys Thr Thr Ile Val Tyr Gly Arg Arg Arg
260 265 270

Ser Lys Ser Arg Glu Arg Arg Ala Pro Thr Pro Gln Arg Ala Gly Ser
275 280 285

Pro Leu Pro Arg Thr Ser Arg Asp His His Arg Ser Pro Ser Pro Arg
290 295 300

Glu
305

<210> 139

<211> 212

<212> PRT

<213> Haemophilus influenzae

<400> 139

Met Lys Lys Thr Leu Leu Gly Ser Leu Ile Leu Leu Ala Phe Ala Gly
1 5 10 15

Asn Val Gln Ala Ala Ala Asn Ala Asp Thr Ser Gly Thr Val Thr Phe
20 25 30

Phe Gly Lys Val Val Glu Asn Thr Cys Gln Val Asn Gln Asp Ser Glu
35 40 45

Tyr Glu Cys Asn Leu Asn Asp Val Gly Lys Asn His Leu Ser Gln Gln
50 55 60

Gly Tyr Thr Ala Met Gln Thr Pro Phe Thr Ile Thr Leu Glu Asn Cys
65 70 75 80

Asn Val Thr Thr Asn Asn Lys Pro Lys Ala Thr Lys Val Gly Val
85 90 95

Tyr Phe Tyr Ser Trp Glu Ile Ala Asp Lys Asp Asn Lys Tyr Thr Leu
100 105 110

Lys Asn Ile Lys Glu Asn Thr Gly Thr Asn Asp Ser Ala Asn Lys Val
115 120 125

Asn Ile Gln Leu Leu Glu Asp Asn Gly Thr Ala Glu Ile Lys Val Val
130 135 140

Gly Lys Thr Thr Asp Phe Thr Ser Glu Asn His Asn Gly Ala Gly
145 150 155 160

Ala Asp Pro Val Ala Thr Asn Lys His Ile Ser Ser Leu Thr Pro Leu
165 170 175

Asn Asn Gln Asn Ser Ile Asn Leu His Tyr Ile Ala Gln Tyr Tyr Ala
180 185 190

Thr Gly Val Ala Glu Ala Gly Lys Val Pro Ser Ser Val Asn Ser Gln
195 200 205

Ile Ala Tyr Glu
210

<210> 140
<211> 139
<212> PRT
<213> *Pseudomonas stutzeri*

<400> 140
Met Lys Ala Gln Met Gln Lys Gly Phe Thr Leu Ile Glu Leu Met Ile
1 5 10 15

Val Val Ala Ile Ile Gly Ile Leu Ala Ala Ile Ala Leu Pro Ala Tyr
20 25 30

Gln Asp Tyr Thr Val Arg Ser Asn Ala Ala Ala Ala Leu Ala Glu Ile
35 40 45

Thr Pro Gly Lys Ile Gly Phe Glu Gln Ala Ile Asn Glu Gly Lys Thr
50 55 60

Pro Ser Leu Thr Ser Thr Asp Glu Gly Tyr Ile Gly Ile Thr Asp Ser
65 70 75 80

Thr Ser Tyr Cys Asp Val Asp Leu Asp Thr Ala Ala Asp Gly His Ile
85 90 95

Glu Cys Thr Ala Lys Gly Gly Asn Ala Gly Lys Phe Asp Gly Lys Thr
100 105 110

Ile Thr Leu Asn Arg Thr Ala Asp Gly Glu Trp Ser Cys Ala Ser Thr
115 120 125

Leu Asp Ala Lys Tyr Lys Pro Gly Lys Cys Ser
130 135

<210> 141
<211> 59
<212> PRT
<213> *Caulobacter crescentus*

<400> 141
Met Thr Lys Phe Val Thr Arg Phe Leu Lys Asp Glu Ser Gly Ala Thr
1 5 10 15

Ala Ile Glu Tyr Gly Leu Ile Val Ala Leu Ile Ala Val Val Ile Val
20 25 30

Thr Ala Val Thr Thr Leu Gly Thr Asn Leu Arg Thr Ala Phe Thr Lys
35 40 45

Ala Gly Ala Ala Val Ser Thr Ala Ala Gly Thr
50 55

<210> 142
<211> 173
<212> PRT
<213> Escherichia coli

<400> 142
Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Ile Pro Gln
1 5 10 15

Gly Gln Gly Lys Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys
20 25 30
Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu
35 40 45

Ser Lys Ser Phe Leu Glu Ala Gly Gly Val Ser Lys Pro Met Asp Leu
50 55 60

Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Gly Gly Asn
65 70 75 80

Gly Ala Gln Lys Gly Thr Val Lys Leu Ala Phe Thr Gly Pro Ile Val
85 90 95

Asn Gly His Ser Asp Glu Leu Asp Thr Asn Gly Gly Thr Gly Thr Ala
100 105 110

Ile Val Val Gln Gly Ala Gly Lys Asn Val Val Phe Asp Gly Ser Glu
115 120 125

Gly Asp Ala Asn Thr Leu Lys Asp Gly Glu Asn Val Leu His Tyr Thr
130 135 140

Ala Val Val Lys Lys Ser Ser Ala Val Gly Ala Ala Val Thr Glu Gly
145 150 155 160

Ala Phe Ser Ala Val Ala Asn Phe Asn Leu Thr Tyr Gln
165 170

<210> 143
<211> 173
<212> PRT
<213> Escherichia coli

<400> 143
Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Ile Pro Gln
1 5 10 15

Gly Gln Gly Lys Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys
20 25 30
Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu
35 40 45

Ser Lys Ser Phe Leu Glu Ala Gly Gly Val Ser Lys Pro Met Asp Leu
50 55 60

Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Gly Gly Asn
65 70 75 80

Gly Ala Gln Lys Gly Thr Val Lys Leu Ala Phe Thr Gly Pro Ile Val
85 90 95

Asn Gly His Ser Asp Glu Leu Asp Thr Asn Gly Gly Thr Gly Thr Ala
100 105 110

Ile Val Val Gln Gly Ala Gly Lys Asn Val Val Phe Asp Gly Ser Glu
115 120 125

Gly Asp Ala Asn Thr Leu Lys Asp Gly Glu Asn Val Leu His Tyr Thr
130 135 140

Ala Val Val Lys Lys Ser Ser Ala Val Gly Ala Ala Val Thr Glu Gly
145 150 155 160
Ala Phe Ser Ala Val Ala Asn Phe Asn Leu Thr Tyr Gln
165 170

<210> 144

<211> 172

<212> PRT

<213> Escherichia coli

<400> 144

Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Thr Pro Gln
1 5 10 15

Gly Gln Gly Arg Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys
20 25 30

Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu
35 40 45

Ser Lys Ser Phe Leu Ala Asn Asp Gly Gln Ser Lys Pro Met Asn Leu
50 55 60

Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Asn Gly Asn
65 70 75 80

Ala Lys Thr Gly Ser Val Lys Leu Ala Phe Thr Gly Pro Thr Val Ser
85 90 95

Gly His Pro Ser Glu Leu Ala Thr Asn Gly Gly Pro Gly Thr Ala Ile
100 105 110

Met Ile Gln Ala Ala Gly Lys Asn Val Pro Phe Asp Gly Thr Glu Gly
115 120 125

Asp Pro Asn Leu Leu Lys Asp Gly Asp Asn Val Leu His Tyr Thr Thr
130 135 140

Val Gly Lys Lys Ser Ser Asp Gly Asn Ala Gln Ile Thr Glu Gly Ala
145 150 155 160

Phe Ser Gly Val Ala Thr Phe Asn Leu Ser Tyr Gln
165 170

<210> 145

<211> 853

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (281)..(829)

<400> 145
acgtttctgt ggctcgacgc atttcctca ttcttctctc caaaaaccac ctcatgcaat 60
ataaaacatct ataaataaaag ataacaataa gaatattaag ccaacaaata aactgaaaaa 120
gtttgtccgc gatgcttac ctctatgagt caaaaatggcc ccaatgttc atctttggg 180
ggaaaactgtg cagtgttgc agtcaaactc gttgacaaac aaagtgtaca gaacgactgc 240
ccatgtcgat ttagaaatag tttttgaaa ggaaagcagc atg aaa att aaa act 295
Met Lys Ile Lys Thr
1 5
ctg gca atc gtt gtt ctg tcg gct ctg tcc ctc agt tct acg acg gct 343
Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu Ser Thr Thr Ala
10 15 20
ctg gcc gct gcc acg acg gtt aat ggt ggg acc gtt cac ttt aaa ggg 391
Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr Val His Phe Lys Gly
25 30 35
gaa gtt gtt aac gcc gct tgc gca gtt gat gca ggc tct gtt gat caa 439
Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala Gly Ser Val Asp Gln
40 45 50
acc gtt cag tta gga cag gtt cgt acc gca tcg ctg gca cag gaa gga 487
Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser Leu Ala Gln Glu Gly
55 60 65
gca acc agt tct gtc ggt ttt aac att cag ctg aat gat tgc gat 535
Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln Leu Asn Asp Cys Asp
70 75 80 85
acc aat gtt gca tct aaa gcc gct gtt gcc ttt tta ggt acg gcg att 583
Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe Leu Gly Thr Ala Ile
90 95 100
gat gcg ggt cat acc aac gtt ctg gct ctg cag agt tca gct gcg ggt 631
Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln Ser Ser Ala Ala Gly
105 110 115
agc gca aca aac gtt ggt gtg cag atc ctg gac aga acg ggt gct gcg 679
Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp Arg Thr Gly Ala Ala
120 125 130
ctg acg ctg gat ggt gcg aca ttt agt tca gaa aca acc ctg aat aac 727
Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu Thr Thr Leu Asn Asn
135 140 145
gga acc aat acc att ccg ttc cag gcg cgt tat ttt gca acc ggg gcc 775
Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr Phe Ala Thr Gly Ala
150 155 160 165
gca acc ccg ggt gct gct aat gcg gat gcg acc ttc aag gtt cag tat 823
Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr Phe Lys Val Gln Tyr
170 175 180
caa taa cctacctagg ttcagggacg ttca 853
Gln

<210> 146
<211> 182
<212> PRT

<213> Escherichia coli

<400> 146
Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu
1 5 10 15
Ser Ser Thr Thr Ala Leu Ala Ala Thr Thr Val Asn Gly Gly Thr
20 25 30
Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala
35 40 45
Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser
50 55 60
Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln
65 70 75 80
Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe
85 90 95
Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln
100 105 110
Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp
115 120 125
Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu
130 135 140
Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr
145 150 155 160
Phe Ala Thr Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr
165 170 175
Phe Lys Val Gln Tyr Gln
180

<210> 147

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FLAG peptide

<400> 147

Cys Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys
1 5 10

<210> 148

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 148

ccggattca tggacattga cccttataaa g

31

<210> 149

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 149
gtgcagtatg gtgaggtgag gaatgctcag gagactc 37

<210> 150
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 150
gsgtctcctg agcattcctc acctcaccat actgcac 37

<210> 151
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 151
cttccaaaag tgagggaaaga aatgtgaaac cac 33

<210> 152
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 152
cgcgtcccaa gcttctaaac aacagtagtc tccggaagcg ttgata 47

<210> 153
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 153
gtggtttcac atttcttccc tcactttgg aag 33

<210> 154
<211> 281
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 154
Met Ser Glu Tyr Gln Pro Ser Leu Phe Ala Leu Asn Pro Met Gly Phe
1 5 10 15

Ser Pro Leu Asp Gly Ser Lys Ser Thr Asn Glu Asn Val Ser Ala Ser
20 25 30

Thr Ser Thr Ala Lys Pro Met Val Gly Gln Leu Ile Phe Asp Lys Phe
35 40 45

Ile Lys Thr Glu Glu Asp Pro Ile Ile Lys Gln Asp Thr Pro Ser Asn
50 55 60

Leu Asp Phe Asp Phe Ala Leu Pro Gln Thr Ala Thr Ala Pro Asp Ala
65 70 75 80

Lys Thr Val Leu Pro Ile Pro Glu Leu Asp Asp Ala Val Val Glu Ser
85 90 95

Phe Phe Ser Ser Ser Thr Asp Ser Thr Pro Met Phe Glu Tyr Glu Asn
100 105 110

Leu Glu Asp Asn Ser Lys Glu Trp Thr Ser Leu Phe Asp Asn Asp Ile
115 120 125

Pro Val Thr Thr Asp Asp Val Ser Leu Ala Asp Lys Ala Ile Glu Ser
130 135 140

Thr Glu Glu Val Ser Leu Val Pro Ser Asn Leu Glu Val Ser Thr Thr
145 150 155 160

Ser Phe Leu Pro Thr Pro Val Leu Glu Asp Ala Lys Leu Thr Gln Thr
165 170 175

Arg Lys Val Lys Lys Pro Asn Ser Val Val Lys Lys Ser His His Val
180 185 190

Gly Lys Asp Asp Glu Ser Arg Leu Asp His Leu Gly Val Val Ala Tyr
195 200 205

Asn Arg Lys Gln Arg Ser Ile Pro Leu Ser Pro Ile Val Pro Glu Ser
210 215 220

Ser Asp Pro Ala Ala Leu Lys Arg Ala Arg Asn Thr Glu Ala Ala Arg
225 230 235 240

Arg Ser Arg Ala Arg Lys Leu Gln Arg Met Lys Gln Leu Glu Asp Lys
245 250 255

Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val Ala
260 265 270

Arg Leu Lys Lys Leu Val Gly Glu Arg
275 280

<210> 155
<211> 181
<212> PRT
<213> Escherichia coli

<400> 155
Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu
1 5 10 15

Ser Ser Thr Ala Ala Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr
20 25 30

Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala
35 40 45.

Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser
50 55 60

Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln
65 70 75 80

Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe
85 90 95

Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln
100 105 110

Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp
115 120 125

Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu
130 135 140

Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr
145 150 155 160

Phe Ala Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr Phe
165 170 175

Lys Val Gln Tyr Gln
180

<210> 156

<211> 447

<212> DNA

<213> Hepatitis B

<220>

<221> CDS

<222> (1)..(447)

<400> 156

atg gac att gac cct tat aaa gaa ttt gga gct act gtg gag tta ctc 48
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

tcg ttt ttg cct tct gac ttc ttt cct tcc gta cga gat ctt cta gat 96
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

acc gcc gca gct ctg tat cgg gat gcc tta gag tct cct gag cat tgt 144
Thr Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45

tca cct cac cat act gca ctc agg caa gca att ctt tgc tgg gga gac 192
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

tta atg act cta gct acc tgg gtg ggt act aat tta gaa gat cca gca 240
Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala
65 70 75 80

tct agg gac cta gta gtc agt tat gtc aac act aat gtg ggc cta aag 288
Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys
85 90 95

ttc aga caa tta ttg tgg ttt cac att tct tgt ctc act ttt gga aga 336
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg

100

105

110

gaa acg gtt cta gag tat ttg gtc tct ttt gga gtg tgg att cgc act 384
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

cct cca gcc tat aga cca cca aat gcc cct atc cta tca acg ctt ccg 432
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

gag act act gtt gtt 447
Glu Thr Thr Val Val
145

<210> 157
<211> 149
<212> PRT
<213> Hepatitis B

<400> 157
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val
145

<210> 158
<211> 152
<212> PRT
<213> Hepatitis B

<400> 158
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp

100 200 300 400 500 600 700 800 900 1000

20 25 30

Thr Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Gly Gly
65 70 75 80

Lys Gly Gly Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val
85 90 95

Gly Leu Lys Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr
100 105 110

Phe Gly Arg Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp
115 120 125

Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser
130 135 140

Thr Leu Pro Glu Thr Thr Val Val
145 150

<210> 159
<211> 132
<212> PRT
<213> Bacteriophage Q Beta

<400> 159
Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly Lys
1 5 10 15

Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
20 25 30

Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
35 40 45

Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
50 55 60

Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
65 70 75 80

Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser Phe
85 90 95

Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
100 105 110

Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
115 120 125

Asn Pro Ala Tyr
130

<210> 160
<211> 129
<212> PRT

<213> Bacteriophage R 17

<400> 160

Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asn Asp Gly Gly Thr Gly
1 5 10 15

Asn Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp
20 25 30

Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val
35 40 45

Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val
50 55 60

Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val Ala
65 70 75 80

Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe Ala
85 90 95

Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu
100 105 110

Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile
115 120 125

Tyr

<210> 161

<211> 130

<212> PRT

<213> Bacteriophage fr

<400> 161

Met Ala Ser Asn Phe Glu Glu Phe Val Leu Val Asp Asn Gly Gly Thr
1 5 10 15

Gly Asp Val Lys Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35 40 45

Val Arg Gln Ser Ser Ala Asn Asn Arg Lys Tyr Thr Val Lys Val Glu
50 55 60

Val Pro Lys Val Ala Thr Gln Val Gln Gly Gly Val Glu Leu Pro Val
65 70 75 80

Ala Ala Trp Arg Ser Tyr Met Asn Met Glu Leu Thr Ile Pro Val Phe
85 90 95

Ala Thr Asn Asp Asp Cys Ala Leu Ile Val Lys Ala Leu Gln Gly Thr
100 105 110

Phe Lys Thr Gly Asn Pro Ile Ala Thr Ala Ile Ala Ala Asn Ser Gly
115 120 125

Ile Tyr
130

<210> 162
<211> 130
<212> PRT
<213> Bacteriophage GA

<400> 162

Met Ala Thr Leu Arg Ser Phe Val Leu Val Asp Asn Gly Gly Thr Gly
1 5 10 15

Asn Val Thr Val Val Pro Val Ser Asn Ala Asn Gly Val Ala Glu Trp
20 25 30

Leu Ser Asn Asn Ser Arg Ser Gln Ala Tyr Arg Val Thr Ala Ser Tyr
35 40 45

Arg Ala Ser Gly Ala Asp Lys Arg Lys Tyr Ala Ile Lys Leu Glu Val
50 55 60

Pro Lys Ile Val Thr Gln Val Val Asn Gly Val Glu Leu Pro Gly Ser
65 70 75 80

Ala Trp Lys Ala Tyr Ala Ser Ile Asp Leu Thr Ile Pro Ile Phe Ala
85 90 95

Ala Thr Asp Asp Val Thr Val Ile Ser Lys Ser Leu Ala Gly Leu Phe
100 105 110

Lys Val Gly Asn Pro Ile Ala Glu Ala Ile Ser Ser Gln Ser Gly Phe
115 120 125

Tyr Ala
130

<210> 163
<211> 132
<212> PRT
<213> Bacteriophage SP

<400> 163

Met Ala Lys Leu Asn Gln Val Thr Leu Ser Lys Ile Gly Lys Asn Gly
1 5 10 15

Asp Gln Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly
20 25 30

Val Ala Ser Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
35 40 45

Val Thr Val Ser Val Ala Gln Pro Ser Arg Asn Arg Lys Asn Phe Lys
50 55 60

Val Gln Ile Lys Leu Gln Asn Pro Thr Ala Cys Thr Arg Asp Ala Cys
65 70 75 80

Asp Pro Ser Val Thr Arg Ser Ala Phe Ala Asp Val Thr Leu Ser Phe
85 90 95
Thr Ser Tyr Ser Thr Asp Glu Glu Arg Ala Leu Ile Arg Thr Glu Leu
100 105 110
Ala Ala Leu Leu Ala Asp Pro Leu Ile Val Asp Ala Ile Asp Asn Leu
115 120 125
Asn Pro Ala Tyr
130

<210> 164
<211> 130
<212> PRT
<213> Bacteriophage MS2

<400> 164

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1 5 10 15

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
65 . 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
115 120 125

Ile Tyr
130

<210> 165
<211> 133
<212> PRT
<213> Bacteriophage M11

<400> 165
Met Ala Lys Leu Gln Ala Ile Thr Leu Ser Gly Ile Gly Lys Lys Gly
1 5 10 15

Asp Val Thr Leu Asp Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly
20 25 30

Val Ala Ala Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
35 40 45

Val Thr Ile Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
50 55 60

Val Gln Val Lys Ile Gln Asn Pro Thr Ser Cys Thr Ala Ser Gly Thr
65 70 75 80

Cys Asp Pro Ser Val Thr Arg Ser Ala Tyr Ser Asp Val Thr Phe Ser
85 90 95

Phe Thr Gln Tyr Ser Thr Val Glu Glu Arg Ala Leu Val Arg Thr Glu
100 105 110

Leu Gln Ala Leu Leu Ala Asp Pro Met Leu Val Asn Ala Ile Asp Asn
115 120 125

Leu Asn Pro Ala Tyr
130

<210> 166
<211> 133
<212> PRT
<213> Bacteriophage MX1

<400> 166
Met Ala Lys Leu Gln Ala Ile Thr Leu Ser Gly Ile Gly Lys Asn Gly
1 5 10 15

Asp Val Thr Leu Asn Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly
20 25 30

Val Ala Ala Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
35 40 45

Val Thr Ile Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
50 55 60

Val Gln Val Lys Ile Gln Asn Pro Thr Ser Cys Thr Ala Ser Gly Thr
65 70 75 80

Cys Asp Pro Ser Val Thr Arg Ser Ala Tyr Ala Asp Val Thr Phe Ser
85 90 95

Phe Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Leu Val Arg Thr Glu
100 105 110

Leu Lys Ala Leu Leu Ala Asp Pro Met Leu Ile Asp Ala Ile Asp Asn
115 120 125

Leu Asn Pro Ala Tyr
130

<210> 167
<211> 330
<212> PRT
<213> Bacteriophage NL95

<400> 167
Met Ala Lys Leu Asn Lys Val Thr Leu Thr Gly Ile Gly Lys Ala Gly
1 5 10 15

Asn Gln Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly

	20	25	30
Val Ala Ser Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg			
35	40	45	
Val Thr Val Ser Val Ala Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys			
50	55	60	
Val Gln Ile Lys Leu Gln Asn Pro Thr Ala Cys Thr Lys Asp Ala Cys			
65	70	75	80
Asp Pro Ser Val Thr Arg Ser Gly Ser Arg Asp Val Thr Leu Ser Phe			
85	90	95	
Thr Ser Tyr Ser Thr Glu Arg Glu Arg Ala Leu Ile Arg Thr Glu Leu			
100	105	110	
Ala Ala Leu Leu Lys Asp Asp Leu Ile Val Asp Ala Ile Asp Asn Leu			
115	120	125	
Asn Pro Ala Tyr Trp Ala Ala Leu Leu Ala Ala Ser Pro Gly Gly Gly			
130	135	140	
Asn Asn Pro Tyr Pro Gly Val Pro Asp Ser Pro Asn Val Lys Pro Pro			
145	150	155	160
Gly Gly Thr Gly Thr Tyr Arg Cys Pro Phe Ala Cys Tyr Arg Arg Gly			
165	170	175	
Glu Leu Ile Thr Glu Ala Lys Asp Gly Ala Cys Ala Leu Tyr Ala Cys			
180	185	190	
Gly Ser Glu Ala Leu Val Glu Phe Glu Tyr Ala Leu Glu Asp Phe Leu			
195	200	205	
Gly Asn Glu Phe Trp Arg Asn Trp Asp Gly Arg Leu Ser Lys Tyr Asp			
210	215	220	
Ile Glu Thr His Arg Arg Cys Arg Gly Asn Gly Tyr Val Asp Leu Asp			
225	230	235	240
Ala Ser Val Met Gln Ser Asp Glu Tyr Val Leu Ser Gly Ala Tyr Asp			
245	250	255	
Val Val Lys Met Gln Pro Pro Gly Thr Phe Asp Ser Pro Arg Tyr Tyr			
260	265	270	
Leu His Leu Met Asp Gly Ile Tyr Val Asp Leu Ala Glu Val Thr Ala			
275	280	285	
Tyr Arg Ser Tyr Gly Met Val Ile Gly Phe Trp Thr Asp Ser Lys Ser			
290	295	300	
Pro Gln Leu Pro Thr Asp Phe Thr Arg Phe Asn Arg His Asn Cys Pro			
305	310	315	320
Val Gln Thr Val Ile Val Ile Pro Ser Leu			
325	330		

<210> 168
<211> 134
<212> PRT

<213> Apis mellifera

<400> 168
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
1 5 10 15

Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
20 25 30

Thr His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
35 40 45
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
50 55 60

Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser
65 70 75 80

Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
85 90 95

Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
100 105 110

Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
115 120 125

Phe Asp Leu Arg Lys Tyr
130

<210> 169

<211> 129

<212> PRT

<213> Apis mellifera

<400> 169
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
1 5 10 15

Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
20 25 30

Thr His Asp Met Cys Pro Asn Val Met Ser Ala Gly Glu Ser Lys His
35 40 45

Gly Leu Thr Asp Thr Ala Ser Arg Leu Ser Cys Asn Asp Asn Asp Leu
50 55 60

Phe Tyr Lys Asp Ser Ala Asp Thr Ile Ser Ser Tyr Phe Val Gly Lys
65 70 75 80

Met Tyr Phe Asn Leu Ile Asn Thr Lys Cys Tyr Lys Leu Glu His Pro
85 90 95

Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg Cys Leu His Tyr Thr
100 105 110

Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp Phe Asp Leu Arg Lys
115 120 125

Tyr

<210> 170
<211> 134
<212> PRT
<213> Apis dorsata

<400> 170
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Val Ser Ser
1 5 10 15
Ser Pro Asp Glu Leu Gly Arg Phe Lys His Thr Asp Ser Cys Cys Arg
20 25 30
Ser His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
35 40 45
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
50 55 60
Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ser Asp Thr Ile Ser Ser
65 70 75 80
Tyr Phe Val Gly Glu Met Tyr Phe Asn Ile Leu Asp Thr Lys Cys Tyr
85 90 95
Lys Leu Glu His Pro Val Thr Gly Cys Gly Lys Arg Thr Glu Gly Arg
100 105 110
Cys Leu Asn Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
115 120 125
Phe Asp Leu Arg Lys Tyr
130

<210> 171
<211> 134
<212> PRT
<213> Apis cerana

<400> 171
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Val Ser Ser
1 5 10 15
Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
20 25 30
Thr His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
35 40 45
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
50 55 60
Asp Thr Phe Tyr Asp Cys Leu Lys Asn Ser Gly Glu Lys Ile Ser Ser
65 70 75 80
Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
85 90 95
Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
100 105 110
Cys Leu Arg Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
115 120 125

Phe Asp Leu Arg Lys Tyr
130

<210> 172
<211> 136
<212> PRT
<213> Bombus pennsylvanicus

<400> 172

Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly Asn Gly Asn Ile Ala Asn
1 5 10 15

Gly Thr Asn Glu Leu Gly Leu Trp Lys Glu Thr Asp Ala Cys Cys Arg
20 25 30

Thr His Asp Met Cys Pro Asp Ile Ile Glu Ala His Gly Ser Lys His
35 40 45

Gly Leu Thr Asn Pro Ala Asp Tyr Thr Arg Leu Asn Cys Glu Cys Asp
50 55 60

Glu Glu Phe Arg His Cys Leu His Asn Ser Gly Asp Ala Val Ser Ala
65 70 75 80

Ala Phe Val Gly Arg Thr Tyr Phe Thr Ile Leu Gly Thr Gln Cys Phe
85 90 95

Arg Leu Asp Tyr Pro Ile Val Lys Cys Lys Val Lys Ser Thr Ile Leu
100 105 110

Arg Glu Cys Lys Glu Tyr Glu Phe Asp Thr Asn Ala Pro Gln Lys Tyr
115 120 125

Gln Trp Phe Asp Val Leu Ser Tyr
130 135

<210> 173
<211> 142
<212> PRT
<213> Heloderma suspectum

<400> 173

Gly Ala Phe Ile Met Pro Gly Thr Leu Trp Cys Gly Ala Gly Asn Ala
1 5 10 15

Ala Ser Asp Tyr Ser Gln Leu Gly Thr Glu Lys Asp Thr Asp Met Cys
20 25 30

Cys Arg Asp His Asp His Cys Ser Asp Thr Met Ala Ala Leu Glu Tyr
35 40 45

Lys His Gly Met Arg Asn Tyr Arg Pro His Thr Val Ser His Cys Asp
50 55 60

Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Asn Val Lys Asp Arg Thr
65 70 75 80

Ala Asp Leu Val Gly Met Thr Tyr Phe Thr Val Leu Lys Ile Ser Cys
85 90 95

Phe Glu Leu Glu Glu Gly Glu Gly Cys Val Asp Asn Asn Phe Ser Gln
100 105 110

Gln Cys Thr Lys Ser Glu Ile Met Pro Val Ala Lys Leu Val Ser Ala
115 120 125

Ala Pro Tyr Gln Ala Gln Ala Glu Thr Gln Ser Gly Glu Gly
130 135 140

<210> 174

<211> 143

<212> PRT

<213> *Heloderma suspectum*

<400> 174

Gly Ala Phe Ile Met Pro Gly Thr Leu Trp Cys Gly Ala Gly Asn Ala
1 5 10 15

Ala Ser Asp Tyr Ser Gln Leu Gly Thr Glu Lys Asp Thr Asp Met Cys
20 25 30

Cys Arg Asp His Asp His Cys Glu Asn Trp Ile Ser Ala Leu Glu Tyr
35 40 45

Lys His Gly Met Arg Asn Tyr Tyr Pro Ser Thr Ile Ser His Cys Asp
50 55 60

Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Lys Leu Lys Asp Gly Thr
65 70 75 80

Ala Asp Tyr Val Gly Gln Thr Tyr Phe Asn Val Leu Lys Ile Pro Cys
85 90 95

Phe Glu Leu Glu Glu Gly Glu Cys Val Asp Trp Asn Phe Trp Leu
100 105 110

Glu Cys Thr Glu Ser Lys Ile Met Pro Val Ala Lys Leu Val Ser Ala
115 120 125

Ala Pro Tyr Gln Ala Gln Ala Glu Thr Gln Ser Gly Glu Gly Arg
130 135 140

<210> 175

<211> 142

<212> PRT

<213> *Heloderma suspectum*

<400> 175

Gly Ala Phe Ile Met Pro Gly Thr Leu Trp Cys Gly Ala Gly Asn Ala
1 5 10 15

Ala Ser Asp Tyr Ser Gln Leu Gly Thr Glu Lys Asp Thr Asp Met Cys
20 25 30

Cys Arg Asp His Asp His Cys Glu Asn Trp Ile Ser Ala Leu Glu Tyr
35 40 45

Lys His Gly Met Arg Asn Tyr Tyr Pro Ser Thr Ile Ser His Cys Asp
50 55 60

Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Lys Leu Lys Asp Gly Thr

65 70 75 80
Ala Asp Tyr Val Gly Gln Thr Tyr Phe Asn Val Leu Lys Ile Pro Cys
85 90 95
Phe Glu Leu Glu Glu Gly Cys Val Asp Trp Asn Phe Trp Leu
100 105 110
Glu Cys Thr Glu Ser Lys Ile Met Pro Val Ala Lys Leu Val Ser Ala
115 120 125
Ala Pro Tyr Gln Ala Gln Ala Glu Thr Gln Ser Gly Glu Gly
130 135 140

<210> 176
<211> 574
<212> PRT
<213> IgE heavy chain

<400> 176

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Gln Thr Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro
20 25 30

Gly Ala Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile
35 40 45

Asp Ser Tyr Ile His Trp Ile Arg Gln Ala Pro Gly His Gly Leu Glu
50 55 60

Trp Val Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Pro
65 70 75 80

Arg Phe Gln Gly Arg Val Thr Met Thr Arg Asp Ala Ser Phe Ser Thr
85 90 95

Ala Tyr Met Asp Leu Arg Ser Leu Arg Ser Asp Asp Ser Ala Val Phe
100 105 110

Tyr Cys Ala Lys Ser Asp Pro Phe Trp Ser Asp Tyr Tyr Asn Phe Asp
115 120 125

Tyr Ser Tyr Thr Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
130 135 140

Ser Ser Ala Ser Thr Gln Ser Pro Ser Val Phe Pro Leu Thr Arg Cys
145 150 155 160

Cys Lys Asn Ile Pro Ser Asn Ala Thr Ser Val Thr Leu Gly Cys Leu
165 170 175

Ala Thr Gly Tyr Phe Pro Glu Pro Val Met Val Thr Trp Asp Thr Gly
180 185 190

Ser Leu Asn Gly Thr Thr Met Thr Leu Pro Ala Thr Thr Leu Thr Leu
195 200 205

Ser Gly His Tyr Ala Thr Ile Ser Leu Leu Thr Val Ser Gly Ala Trp
210 215 220

Ala Lys Gln Met Phe Thr Cys Arg Val Ala His Thr Pro Ser Ser Thr
225 230 235 240

Asp Trp Val Asp Asn Lys Thr Phe Ser Val Cys Ser Arg Asp Phe Thr
245 250 255

Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly Gly His
260 265 270

Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr Thr Pro
275 280 285

Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met Asp Val
290 295 300

Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala Ser Thr
305 310 315 320

Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp Arg Thr
325 330 335

Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp Ser Thr
340 345 350

Lys Lys Cys Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser
355 360 365

Arg Pro Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr Ile Thr
370 375 380

Cys Leu Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr
385 390 395 400

Trp Ser Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu
405 410 415

Glu Lys Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val
420 425 430

Gly Thr Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr
435 440 445

His Pro His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser
450 455 460

Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp
465 470 475 480

Pro Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln Asn Phe
485 490 495

Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln Leu
500 505 510

Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser
515 520 525

Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp Glu
530 535 540

Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro
545 550 555 560

Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys
565 570

<210> 177

<400> 177
000

<210> 178
<211> 13
<212> PRT
<213> IgE Peptides

<400> 178
Cys Gly Gly Val Asn Leu Thr Trp Ser Arg Ala Ser Gly
1 5 10

<210> 179
<211> 8
<212> PRT
<213> IgE Mimotype

<400> 179
Ile Asn His Arg Gly Tyr Trp Val
1 5

<210> 180
<211> 8
<212> PRT
<213> IgE Mimotype

<400> 180
Arg Asn His Arg Gly Tyr Trp Val
1 5

<210> 181
<211> 10
<212> PRT
<213> IgE Mimotype

<400> 181

Arg Ser Arg Ser Gly Gly Tyr Trp Leu Trp
1 5 10

<210> 182
<211> 10
<212> PRT
<213> IgE Mimotype

<400> 182
Val Asn Leu Thr Trp Ser Arg Ala Ser Gly
1 5 10

<210> 183
<211> 10
<212> PRT
<213> IgE Mimotype

<400> 183
Val Asn Leu Pro Trp Ser Arg Ala Ser Gly
1 5 10

<210> 184
<211> 10
<212> PRT
<213> IgE Mimotype

<400> 184
Val Asn Leu Thr Trp Ser Phe Gly Leu Glu
1 5 10

<210> 185
<211> 10
<212> PRT
<213> IgE Mimotype

<400> 185
Val Asn Leu Pro Trp Ser Phe Gly Leu Glu
1 5 10

<210> 186
<211> 10
<212> PRT
<213> IgE Mimotype

<400> 186
Val Asn Arg Pro Trp Ser Phe Gly Leu Glu
1 5 10

<210> 187
<211> 10
<212> PRT
<213> IgE Mimotype

<400> 187
Val Lys Leu Pro Trp Arg Phe Tyr Gln Val
1 5 10

<210> 188
<211> 10
<212> PRT
<213> IgE Mimotype

<400> 188
Val Trp Thr Ala Cys Gly Tyr Gly Arg Met
1 5 10

<210> 189
<211> 7

<212> PRT
<213> IgE Mimotype

<400> 189
Gly Thr Val Ser Thr Leu Ser
1 5

<210> 190
<211> 7
<212> PRT
<213> IgE Mimotype

<400> 190
Leu Leu Asp Ser Arg Tyr Trp
1 5

<210> 191
<211> 7
<212> PRT
<213> IgE Mimotype

<400> 191
Gln Pro Ala His Ser Leu Gly
1 5

<210> 192
<211> 7
<212> PRT
<213> IgE Mimotype

<400> 192
Leu Trp Gly Met Gln Gly Arg
1 5

<210> 193
<211> 15
<212> PRT
<213> IgE Mimotype

<400> 193
Leu Thr Leu Ser His Pro His Trp Val Leu Asn His Phe Val Ser
1 5 10 15

<210> 194
<211> 9
<212> PRT
<213> IgE Mimotype

<400> 194
Ser Met Gly Pro Asp Gln Thr Leu Arg
1 5

<210> 195
<211> 6
<212> PRT
<213> IgE Mimotype

<400> 195
Val Asn Leu Thr Trp Ser
1 5

<210> 196
<211> 56
<212> DNA
<213> Oligonucleotide Primer

<400> 196
tagatgatta cgccaagctt ataatagaaa tagtttttg aaaggaaagc agcatg 56

<210> 197
<211> 45
<212> DNA
<213> Oligonucleotide Primer

<400> 197
gtcaaaggcc ttgtcgacgt tattccatta cggccgtcat tttgg 45

<210> 198
<211> 4623
<212> DNA
<213> pFIMAIC

<400> 198
agacgaaagg gcctcggtat acgcctattt ttataggta atgtcatgtat aataatggtt 60
tcttagacgt caggtggcac tttcgggaa aatgtgcgcg gaaccctat ttgtttattt 120
ttctaaatac attcaaataat gtatccgctc atgagacaat aaccctgata aatgcttcaa 180
taatattgaa aaaggaagag tatgagtatt caacatttcc gtgtcgccct tattcccttt 240
tttgcggcat tttgccttcc tggatcttgcgtt caccagaaa cgctggtgaa agtaaaagat 300
gctgaagatc agttgggtgc acgagtgggt tacatcgaaac tggatctcaa cagcggtaag 360
atccttggaga gtttcgccc cgaagaacgt tttccatga tgagcacttt taaagttctg 420
ctatgtggcg cggattatc ccgtatttgc gcccggcaag agcaactcg tcgcccgcata 480
caacttctc agaatgactt ggttggatc tcaccagtca cagaaaagca tcttacggat 540
ggcatgacag taagagaatt atgcagtgtt gccataacca tgagtataa cactgcggcc 600
aacttacttc tgacaacgtat cggaggaccg aaggagctaa ccgtttttt gcacaacatg 660
ggggatcatg taactcgccct tgatcggtgg gaaccggagc tgaatgaagc cataccaaac 720
gacgagcgtg acaccacgtat gcctgttagca atggcaacaa cgttgcgcaa actattaact 780
ggcgaactac ttactcttagc ttcccgccaa caatataatag actggatgga ggcggataaa 840

gttgcaggac cacttctgct ctcggccctt ccggctggct ggtttattgc tgataaaatct 900
ggagccggtg agcgtggtc tcgcggatc attgcagcac tggggccaga tggtaagccc 960
tcccgtatcg tagttatcta cacgacgggg agtcaggcaa ctatggatga acgaaataga 1020
cagatcgctg agataggtgc ctcactgatt aagcattggt aactgtcaga ccaagttac 1080
tcatatatac tttagattga tttaaaactt catttttaat ttaaaaggat ctaggtgaag 1140
atccttttg ataatctcat gacaaaatc ccttaacgtg agtttcgtt ccactgagcg 1200
tcagaccccg tagaaaagat caaaggatct tcttgagatc cttttttct ggcgtaatc 1260
tgctgcttgc aaacaaaaaa accaccgcta ccagcggtgg tttgttgcc ggatcaagag 1320
ctaccaactc ttttccgaa ggttaactggc ttcagcagag cgccagatacc aaatactgtc 1380
cttctagtgt agccgtagtt aggccaccac ttcaagaact ctgtagcacc gcctacatac 1440
ctcgctctgc taatcctgtt accagtggct gctgccagtg gcgataagtc gtgtcttacc 1500
gggttggact caagacgata gttaccggat aaggcgcagc ggtcgggctg aacgggggt 1560
tcgtgcacac agccagctt ggagcgaacg acctacaccg aactgagata cctacagcgt 1620
gagctatgag aaagcgccac gcttccgaa gggagaaagg cggacaggta tccggtaagc 1680
ggcagggtcg gaacaggaga gcgcacgagg gagcttccag gggaaacgc ctggtatctt 1740
tatagtcctg tcgggtttcg ccacctctga cttagcgtc gatTTTgtg atgctcgtca 1800
ggggggcgga gcctatggaa aaacgcccagc aacgcggcct tttacggtt cctggcctt 1860
tgctggcctt ttgctcacat gtttttccct gcgttatccc ctgattctgt ggataaccgt 1920
attaccgcct ttgagtgagc tgataaccgtc cgccgcagcc gaacgaccga ggcgcagc 1980
tcagtgagcg aggaagcgga agagcgccca atacgcaaacc cgcctctccc cgccgcgttgg 2040
ccgattcatt aatgcagctg gcacgacagg tttccgact ggaaagcggg cagtgagcgc 2100
aacgcaatta atgtgagttt gctcactcat taggcacccc aggcttaca ctttatgctt 2160
ccggctcgta tttttgtgg aattgtgagc ggataacaat ttcacacagg aaacagctat 2220
gaccatgatt acgccaagct tataatagaa atagttttt gaaagggaaag cagcatgaaa 2280
ataaaaactc tggcaatcgt ttttctgtcg gctctgtccc tcagttctac agcggctctg 2340
gccgctgcca cgacggtaa tgggggacc gttcacttta aaggggaagt ttttaacgc 2400
gtttgcgcag ttgatgcagg ctctgttgc caaaccgttc agttaggaca gtttgcgtacc 2460
gcacgcgtgg cacaggaagg agcaaccagt tctgcgtcg gttttaacat tcagctgaat 2520
gattgcgata ccaatgtgc atctaaagcc gctgttgcct ttttaggtac ggcgattgtat 2580
gcgggtcata ccaacgttct ggctctgcag agtcagctg cgggtagcgc aacaaacgtt 2640
ggtgtgcaga tcctggacag aacgggtgct ggcgtgacgc tggatggtgc gacatttagt 2700
tcagaaacaa ccctgaataa cggAACCAAT accattccgt tccaggcgcg ttatTTGCA 2760

accggggccg caaccccccggg tgctgcta at gcggatgcga cttcaaggt tcagtatcaa 2820
taacctaccc agttcaggg acgtcattac gggcagggat gcccaccctt gtgcgataaa 2880
aataacgatg aaaaggaaga gattatttctt attagcgtcg ttgctgcca tgtttgctct 2940
ggccggaaat aaatggaata ccacgttgcc cgccggaaat atgcaatttc agggcgtcat 3000
tattgcgaa acttgccgga ttgaagccgg tgataaacaa atgacggtca atatgggca 3060
aatcagcagt aaccggtttc atgcgggtgg ggaagatagc gcaccgggtgc cttttgttat 3120
tcatttacgg gaatgttagca cgggtggtag tgaacgtgta ggtgtggcgt ttcacgggt 3180
cgccggatggt aaaaatccgg atgtgcttcc cgtgggagag gggccaggga tagccaccaa 3240
tattggcgta gcgttggttt atgatgaagg aaacctcgta ccgattaatc gtcctccagc 3300
aaactggaaa cggctttatt caggctctac ttgcctacat ttcatcgcca aatatcgtgc 3360
taccgggcgt cgggttactg gcggcatcgc caatgcccag gcctgggtct cttaaccta 3420
tcagtaatttgc ttcagcagat aatgtgataa caggaacagg acagttagtataaaaaacgt 3480
caatgtaaagg aaatcgcagg aaataacatt ctgcttgctg gcaggtatcc tgatgttcat 3540
ggcaatgtatg gttgccggac gcgctgaagc gggagtgcc tttaggtgcga ctcgcgtat 3600
ttatccggca gggcaaaaac aagagcaact tgccgtgaca aataatgtatg aaaatagtac 3660
ctattnaattt caatcatggg tggaaaatgc cgatgggtgta aaggatggtc gttttatcgt 3720
gacgccttctt ctgtttgcga tgaagggaaa aaaagagaat accttacgta ttcttgatgc 3780
aacaataac caattgccac aggaccggga aagtttattc tggatgaacg ttaaagcgat 3840
tccgtcaatg gataaatcaa aattgactga gaatacgcta cagctcgcaa ttatcagccg 3900
cattaaactg tactatcgcc cggctaaattt agcgttgcca cccgatcagg ccgcagaaaa 3960
attnaagattt cgtcgtagcg cgaattctct gacgctgatt aacccgacac cctattacct 4020
gacggtaaca gagttgaatg ccggaaacccg ggttcttgcgaa aatgcattgg tgccctccat 4080
ggccgaaagc acggtaaat tgccttctga tgcaggaagc aatattactt accgaacaat 4140
aaatgattat ggccactta cccccaaaat gacggcgta atggaataac gtcgactcta 4200
gaggatcccc gggtaaccgag ctcgaattca ctggccgtcg ttttacaacg tcgtgactgg 4260
gaaaacccctg gcgttaccca acttaatcgc cttgcagcac atccccctt cggcagctgg 4320
cgtaatagcg aagaggcccg caccgatcgc cttcccaac agttgcgcag cctgaatggc 4380
gaatggcgcc tcatgcggta ttttctcctt acgcatctgt gcggtatttc acaccgcata 4440
tgggtgcactc tcagtacaat ctgctctgat gccgcatagt taagccagcc ccgacacccg 4500
ccaaacacccg ctgacgcgccc ctgacgggct tgcgtgcctt cggcatccgc ttacagacaa 4560
gctgtgaccg tctccggag ctgcatgtgt cagaggtttt caccgtcatac accgaaacgc 4620
gcg 4623

<210> 199
<211> 42
<212> DNA
<213> Oligonucleotide Primer

<400> 199
aagatcttaa gcttaagcttg aattctctga cgctgattaa cc * 42

<210> 200
<211> 41
<212> DNA
<213> Oligonucleotide Primer

<400> 200
acgtaaagca tttcttagacc gcggatagta atcgtgctat c 41

<210> 201
<211> 5681
<212> DNA
<213> pFIMD

<400> 201
tcaccgtcat caccgaaacg cgcgagacga aagggcctcg tgatacgcct atttttata 60
gttaatgtca tgataataat ggtttcttag acgtcaggtg gcactttcg gggaaatgt 120
cgcgaaaccc ctatttgtt attttctaa atacattcaa atatgtatcc gctcatgaga 180
caataaccct gataaaatgct tcaataatat tgaaaaagga agagtagttag tattcaacat 240
ttccgtgtcg cccttattcc ctttttgcg gcattttgcc ttccctgttt tgctcaccca 300
gaaacgctgg tgaaagtaaa agatgctgaa gatcagttgg gtgcacgagt gggttacatc 360
gaactggatc tcaacagcgg taagatcctt gagagtttc gccccgaaga acgtttcca 420
atgatgagca cttttaaagt tctgctatgt ggccgcgtat tatccgtat tgacgcccgg 480
caagagcaac tcggtcgccc catacactat tctcagaatg acttgggtga gtactcacca 540
gtcacagaaa agcatcttac ggtatggcatg acagtaagag aattatgcag tgctgccata 600
accatgagtg ataacactgc ggccaactta cttctgacaa cgatcggagg accgaaggag 660
ctaaccgctt tttgcacaa catggggat catgtaactc gccttgatcg ttgggaaccc 720
gagctgaatg aagccatacc aaacgacgag cgtgacacca cgatgcctgt agcaatggca 780
acaacgttgc gcaaactatt aactggcgaa ctacttactc tagttcccg gcaacaatta 840
atagactgga tggaggcgga taaagttgca ggaccacttc tgcgctcgcc cttccggct 900
ggctgggtta ttgctgataa atctggagcc ggtgagcgtg ggtctcgccg tatcattgca 960
gcactggggc cagatggtaa gcccctccgt atcgttagtta tctacacgac ggggagtcag 1020

gcaactatgg atgaacgaaa tagacagatc gctgagatag gtgcctcact gattaagcat 1080
tggtaactgt cagaccaagt ttactcatat atactttaga ttgatttaaa acttcatttt 1140
taatttaaaa ggatcttagt gaagatcctt tttgataatc tcatgaccaa aatcccttaa 1200
cgtgagttt cgttccactg agcgtcagac cccgtagaaa agatcaaagg atcttcttga 1260
gatcctttt ttctgcgcgt aatctgcgtc ttgcaaacaa aaaaaccacc gctaccagcg 1320
gtggtttgg tgcggatca agagctacca actcttttc cgaaggtaac tggttcagc 1380
agagcgcaga taccaaatac tgccttcta gttagccgt agttaggcca ccacttcaag 1440
aactctgtag caccgcctac atacctcgct ctgctaattcc tggttaccagt ggctgctgcc 1500
agtggcgata agtcgtgtct taccgggttg gactcaagac gatagttacc ggataaggcg 1560
cagcggtcgg gctgaacggg gggttcgtgc acacagccca gcttggagcg aacgacctac 1620
accgaactga gatacctaca gcgtgagcta tgagaaagcg ccacgcttcc cgaagggaga 1680
aaggcggaca ggtatccggt aagcggcagg gtcggaacag gagagcgcac gaggagctt 1740
ccagggggaa acgcctggta tctttatagt cctgtcggtt ttcgccccctt ctgacttgag 1800
cgtcgatttt tggatgtcgtc gtcagggggg cggagcctat ggaaaaacgc cagcaacgcg 1860
gccttttac ggttcctggc cttttgctgg cctttgctc acatgttctt tccctgcgtta 1920
tcccctgatt ctgtggataa ccgtattacc gccttgagt gagctgatac cgctcgccgc 1980
agccgaacga ccgagcgcag cgagtcagtg agcgaggaag cggaaagagcg cccaatacgc 2040
aaaccgcctc tccccgcgcg ttggccgatt cattaatgca gctggcacga caggtttccc 2100
gactggaaag cgggcagtga ggcgaacgca attaatgtga gttagctcac tcattaggca 2160
ccccaggctt tacactttat gcttccggct cgtatgttgc gtggaaattgt gagcggataa 2220
caatttcaca cagggaaacag ctatgaccat gattacgcca agcttgaatt ctctgacgct 2280
gattaacccg acaccctatt acctgacggt aacagagttg aatgcccggaa cccgggttct 2340
tgaaaatgca ttgggtgcctc caatggcga aagcacgggtt aaattgcctt ctgatgcagg 2400
aagcaatatt acttaccgaa caataaatga ttatggcga cttaccggaa aaatgacggg 2460
cgtaatggaa taacgcaggg ggaatttttc gcctgaataa aaagaattga ctgcccgggt 2520
gatttttaagc cggaggaata atgtcatatc tgaatttaag actttaccag cggaaacacac 2580
aatgcttgca tattcgtaag catcggttgg ctggttttt tgcgtcgactc gttgtcgctt 2640
gtgctttgc cgcacaggca cctttgtcat ctggcacct ctatggaaat ccgcgttttt 2700
tagcggatga tccccaggct gtggccgatt tatcggttt tgaaaatggg caagaattac 2760
cgccaggac gatcgacgtc gatatctatt tgaataatgg ttatatggca acgcgtgatg 2820
tcacatttaa tacgggcgac agtgaacaag ggattgttcc ctgcctgaca cgcgcgcaac 2880

tcgcccagtat ggggctgaat acggcttctg tcgcccgtat gaatctgctg gcggatgatg 2940
cctgtgtgcc attaaccaca atggtccagg acgctactgc gcatctggat gttggtcagc 3000
agcgactgaa cctgacgatc cctcaggcat ttatgagtaa tcgcgcgcgt gtttatattc 3060
ctcctgagtt atgggatccc ggtattaatg ccggattgct caattataat ttcagcggaa 3120
atagtgtaca gaatcggatt ggggtaaca gccattatgc atattaaac ctacagagt 3180
ggttaaatat tggtgcgtgg cgtttacgcg acaataccac ctggagttat aacagtagcg 3240
acagatcatc aggttagcaaa aataaatggc agcatatcaa tacctggctt gagcgagaca 3300
taataccgtt acgttcccgg ctgacgctgg gtgatggta tactcaggc gatatttcg 3360
atggtattaa ctttcgcggc gcacaattgg cctcagatga caatatgtta cccgatagtc 3420
aaagaggatt tgccccggtg atccacggta ttgctcgtgg tactgcacag gtcactatt 3480
aacaatgg gtatgacatt tataatagta cggtgccacc ggggcctttt accatcaacg 3540
atatctatgc cgccaggtaat agtggtgact tgcaggtAAC gatcaaagag gctgacggca 3600
gcacgcagat ttttaccgta ccctattcgt cagtcggcgt tttgcaacgt gaagggcata 3660
ctcgttattc cattacggca ggagaatacc gtatggaaa tgccgcagcag gaaaaaaaccc 3720
gcttttcca gagtacatta ctccacggcc ttccggctgg ctggacaata tatggtgaa 3780
cgcaactggc ggatcgttat cgtgcttttta atttcggat cggaaaaac atgggggcac 3840
tggcgctct gtctgtggat atgacgcagg ctaattccac acttcccgat gacagtca 3900
atgacggaca atcgggtcgt tttctctata acaaatcgct caatgaatca ggcacgaata 3960
ttcagttagt gggttaccgt tattcgacca gcggatattt taatccgt gatacaacat 4020
acagtcgaat gaatggctac aacattgaaa cacaggacgg agttattcag gtaagccga 4080
aattcaccga ctattacaac ctcgcttata acaaacgcgg gaaattacaa ctcaccgtt 4140
ctcagcaact cggcgcaca tcaacactgt atttgagtg tagccatcaa acttattggg 4200
gaacgagtaa tgcgtatgag caattccagg ctggattaaa tactgcgttc gaagatata 4260
actggacgtc cagctatagc ctgacgaaaa acgcctggca aaaaggacgg gatcagatgt 4320
tagcgcttaa cgtcaatatt ctttcagcc actggctgcg ttctgacagt aaatctcagt 4380
ggcgacatgc cagtgcgcac tacagcatgt cacacgatct caacggcgg atgaccaatc 4440
tggctggtgt atacggtagc ttgctggaaag acaacaacct cagctatagc gtgcaaaccg 4500
gctatgccgg gggaggcgat gaaatagcg gaagtacagg ctacgccacg ctgaattatc 4560
gcgggtgtta cggcaatgcc aatatcggtt acagccatag cgatgatatt aagcagctct 4620
attacggagt cagcggtggg gtactggctc atgccaatgg cgtaacgctg gggcagccgt 4680
taaacgatac ggtggtgctt gttaaagcgc ctggcgcaaa agatgcaaaa gtcgaaaacc 4740
agacgggggt gcgtaccgac tggcgtggtt atgcccgtgct gccttatgcc actgaatatc 4800

gggaaaatag agtggcgctg gataccaata ccctggctga taacgtcgat ttagataacg 4860
cggttgctaa cggtgttccc actcgtgggg cgatcgtgcg agcagagttt aaagcgcg 4920
ttgggataaa actgctcatg acgctgaccc acaataataa gccgctgccc tttggggcga 4980
tggtgacatc agagagtagc cagagtagcg gcattgtgc ggataatggc caggtttacc 5040
tcagcggaat gccttagcg ggaaaagtgc aggtgaaatg gggagaagag gaaaatgctc 5100
actgtgtcgc caattatcaa ctgccaccag agagtcagca gcagttatta acccagctat 5160
cagctgaatg tcgttaaggg ggcgtatga gaaacaaacc ttttatctt ctgtgcgc 5220
ttttgtggct ggcgttgagt cacgcttgg ctgcggatag cacgattact atccgcggc 5280
tagaggatcc ccgggttaccg agctcgaatt cactggccgt cgtttacaa cgtcgtgact 5340
gggaaaaccc tggcgttacc caacttaatc gccttgcagc acatccccct ttcgccagct 5400
ggcgtaatag cgaagaggcc cgccaccgatc gcccttccca acagttgcgc agcctgaatg 5460
gcgaatggcg cctgatgcgg tattttctcc ttacgcatct gtgcggtatt tcacaccgca 5520
tatggtgcac tctcagtaca atctgctctg atgccgcata gttaagccag ccccgacacc 5580
cgccaaacacc cgctgacgctg ccctgacggg cttgtctgct cccggcatcc gttacagac 5640
aagctgtgac cgtctccggg agctgcatgt gtcagagg 5681

<210> 202
<211> 40
<212> DNA
<213> Oligonucleotide Primer

<400> 202
aattacgtga gcaagcttat gagaaacaaa ccttttatac 40

<210> 203
<211> 41
<212> DNA
<213> Oligonucleotide Primer

<400> 203
gactaaggcc tttcttagatt attgataaac aaaagtcacg c 41

<210> 204
<211> 4637
<212> DNA
<213> pFIMFGH

<400> 204
aaaggccctc gtgatacgcc tattttata ggttaatgtc atgataataa tggtttctta 60
gacgtcaggt ggcactttc gggaaatgt gcgcggacc cctattgtt tattttctta 120

aatacattca aatatgtatc cgctcatgag acaataaccc tgataaatgc ttcaataata	180
ttgaaaaagg aagagtatga gtattcaaca tttccgtgtc gcccatttgc cctttttgc	240
ggcattttgc cttcctgttt ttgctcaccc agaaacgctg gtgaaagtaa aagatgctga	300
agatcagttg ggtgcacgag tgggttacat cgaactggat ctcaacagcg gtaagatcct	360
tgagagttt cgccccgaag aacgtttcc aatgatgagc actttaaag ttctgctatg	420
tggcgccgta ttatcccgta ttgacgccgg gcaagagcaa ctcggcgcgc gcatacacta	480
ttctcagaat gacttgggtt agtactcacc agtcacagaa aagcatctt cggatggcat	540
gacagtaaga gaattatgca gtgctgccat aaccatgagt gataacactg cggccaaactt	600
acttctgaca acgatcggag gaccgaagga gctaaccgct ttttgcaca acatggggga	660
tcatgttaact cgccttgcattt gttggaaacc ggagctgaat gaagccatac caaacgacga	720
gcgtgacacc acgatgcctg tagcaatggc aacaacgttg cgcaaactat taactggcga	780
actacttact cttagttccc ggcaacaatt aatagactgg atggaggcgg ataaagttgc	840
aggaccactt ctgcgctcgg cccttccggc tggctggttt attgctgata aatctggagc	900
cggtgagcgt gggtctcgcg gtatcatgc agcaactggg ccagatggta agccctcccg	960
tatcgtagtt atctacacga cggggagtcg ggcaactatg gatgaacgaa atagacagat	1020
cgctgagata ggtgcctcac tgattaagca ttgtaactg tcagaccaag tttactcata	1080
tatacttttag attgatttaa aacttcattt ttaatttaaa aggatctagg tgaagatcct	1140
ttttgataat ctcatgacca aaatccctta acgtgagttt tcgttccact gagcgtcaga	1200
ccccgtagaa aagatcaaag gatcttctt agatcctttt tttctgcgcg taatctgctg	1260
cttgcaaaca aaaaaaccac cgctaccagc ggtggttgt ttgccggatc aagagctacc	1320
aactctttt ccgaaggtaa ctggcttcag cagagcgcag ataccaaata ctgtccttct	1380
agttagccg tagttaggcc accacttcaa gaactctgta gcaccgccta catacctcgc	1440
tctgctaattc ctgttaccag tggctgctgc cagtgccat aagtcgtgtc ttaccgggtt	1500
ggactcaaga cgatagttac cggataaggc gcagcggcgt ggctgaacgg ggggttcgtg	1560
cacacagccc agcttggagc gaacgaccta caccgaactg agataacctac agcgtgagct	1620
atgagaaagc gccacgcttc ccgaagggag aaaggcggac aggtatccgg taagcggcag	1680
ggtcggaaca ggagagcgcgca cgagggagct tccaggggaa aacgcctggat atctttata	1740
tcctgtcggtt ttccgccacc tctgacttga gcgtcgattt ttgtgtatgcgtcagggggg	1800
gcggagccta tggaaaaacg ccagcaacgc ggcctttta cggccctgg ccttttgcgt	1860
gcctttgtt ccatgttctt ttccctgcgtt atccctgat tctgtggata accgtattac	1920
cgccctttagt tgagctgata cccgctcgccg cagccgaacg accgagcgcgca gcgagtcagt	1980
gagcggaggaa gcggaaagagc gcccataacg caaaccgcct ctccccgcgc gttggccgat	2040

tcattaatgc agctggcacg acaggtttcc cgactggaaa gcgggcagtg agcgcaacgc 2100
aattaatgtg agttagctca ctcattaggc accccaggct ttacacttta tgcttccggc 2160
tcgtatgttgc tgtgaaattt tgagcggata acaatttcac acaggaaaca gctatgacca 2220
tgattacgcc aagcttatga gaaacaaacc ttttatctt ctgtgcgcctt ttttggct 2280
ggcggtgagt cacgctttgg ctgcggatag cacgattact atcccgccgt atgtcaggga 2340
taacggctgt agtgtggccg ctgaatcaac caattttact gttgatctga tggaaaacgc 2400
ggcgaagcaa tttaacaaca ttggcgcgac gactcctgtt gttccatttc gtatggct 2460
gtcaccctgt ggtaatgccg tttctgcccgt aaagggtggg tttactggcg ttgcagatag 2520
ccacaatgcc aacctgcttg cacttgaaaa tacggtgtca gcggcttcgg gactggaaat 2580
acagcttctg aatgagcagc aaaatcaaatt accccttaat gctccatcgccgcgttcc 2640
gtggacgacc ctgacgcccgg gtaaaccaaa tacgctgaat ttttacgccc ggctaatggc 2700
gacacaggtg cctgtcactg cggggcatat caatgccacg gctacccctca ctcttgaata 2760
tcagtaactg gagatgctca tgaaatggtg caaacgtggg tatgtattgg cggcaatatt 2820
ggcgctcgca agtgcgacga tacaggcagc cgatgtcacc atcacgggtga acggtaagg 2880
cgtcgccaaa ccgtgtacgg tttccaccac caatgccacg gttgatctcg gcgatcttta 2940
ttctttcagt cttatgtctg ccggggccggc atcggcctgg catgatgttgc cgcttgagg 3000
gactaattgt ccgggtggaa cgtcgagggt cactgccacg ttcagcgggg cagccgacag 3060
taccggatataaaaaacc aggggaccgc gcaaaacatc cagttagac tacaggatga 3120
cagtggcaac acattgaata ctggcgcaac caaaacagtt caggtggatg attcctcaca 3180
atcagcgcac ttcccgttac aggtcagagc attgacagta aatggcggag ccactcagg 3240
aaccattcag gcagtgatta gcatcaccta tacctacagc tgaaccggaa gagatgattt 3300
taatgaaacg agttattacc ctgtttgctg tactgctgat gggctggcgt gtaaatgcct 3360
ggtcattcgc ctgtaaaacc gccaatggta ccgctatccc tattggcggt ggcagcgc 3420
atgtttatgt aaaccttgcg cccgtcgta atgtggggca aaacctggtc gtggatctt 3480
cgacgcaaatt ctttgccat aacgattatc cggaaaccat tacagactat gtcacactgc 3540
aacgaggctc ggcttatggc ggcgtgttat ctaatttttc cgggaccgta aaatatagtg 3600
gcagtagcta tccatttcctt accaccagcg aaacgccgcg cggttttat aattcgagaa 3660
cggataagcc gtggccggc ggcgtttatt tgacgcctgt gagcgtgcg ggcgggggtgg 3720
cgattaaagc tggctcatta attgccgtgc ttatggcgtc acagaccaac aactataaca 3780
gcgatgattt ccagttgtg tggaatattt acgccaataa tgatgtggcgt gtcctactg 3840
gcggctgcga tgtttctgct cgtgtatgtca ccgttactct gccggactac cctgggttcag 3900
tgccaaattcc tcttaccgtt tattgtgcga aaagccaaaa cctggggat tacctctccg 3960

gcacaaccgc agatgcgggc aactcgattt tcaccaatac cgcgtcgaaa tcacctgcac 4020
agggcgtcgg cgtacagttg acgcgcaacg gtacgattat tccagcgaat aacacggat 4080
cgtagggact agtagggact tcggcggtaa gtctggatt aacggcaaataat tatgcacgta 4140
ccggaggggca ggtgactgca gggaaatgtgc aatcgattat tggcgtgact tttgtttatc 4200
aataatctag aggatccccg ggtaccgagc tcgaattcac tggccgtcgat tttacaacgt 4260
cgtgactggg aaaaccctgg cgtaacccaa cttaatcgcc ttgcagcaca tcccccttc 4320
gccagctggc gtaatagcga agaggccgc accgatcgcc cttcccaaca gttgcgcagc 4380
ctgaatggcg aatggcgct gatgcggat tttctcctta cgcatactgtg cggatattca 4440
caccgcataat ggtgcactct cagtaaaatc tgctctgatg ccgcatagtt aagccagccc 4500
cgacacccgc caacacccgc tgacgcgccc tgacgggctt gtctgctccc ggcataccgct 4560
tacagacaag ctgtgaccgt ctccgggagc tgcatgtgtc agaggtttc accgtcatca 4620
ccgaaacgcg cgagacg 4637

<210> 205

<211> 9299

<212> DNA

<213> pFIMAICDFGH

<400> 205

cgagacgaaa gggcctcgat atacgcctat ttttataatgtt taatgtcatg ataataatgg 60
tttcttagac gtcaggtggc acttttcggg gaaatgtgcg cggaaaccctt atttgtttat 120
ttttctaaat acattcaaataat atgtatccgc tcatacgacataaaccctga taaatgcttc 180
aataatattt aaaaaggaag agtatacgat ttcaacatctt ccgtgtcgcc cttattccct 240
ttttgcggc attttgcctt cctgttttg ctcacccaga aacgctggtg aaagtaaaag 300
atgctgaaga tcagttgggt gcacgagtggtt gttacatcgacttggatctc aacagcggtt 360
agatccttga gagtttcgc cccgaagaac gtttccaat gatgagactt tttaaagttc 420
tgctatgtgg cgccgttataa tcccgtattt acggccggca agagcaactc ggtcgccgca 480
tacactattt tcagaatgac ttgggtttagt actcaccagt cacagaaaag catcttacgg 540
atggcatgac agtaagagaa ttatgcagtg ctgccataac catgagtgat aacactgcgg 600
ccaaacttact tctgacaacg atcggaggac cgaaggagct aaccgctttt ttgcacaaca 660
tgggggatca tgtaactcgcc cttgatcgat gggaaaccggaa gctgaatgaa gccataccaa 720
acgacgagcg tgacaccacg atgcctgttagt caatggcaac aacgttgccgaa aactattaa 780
ctggcgaact acttactcta gttcccgcc aacaattaat agactggatg gaggcgat 840

aagttgcagg accacttctg cgctcgcccc ttccggctgg ctggtttatt gctgataaat 900
ctggagccgg tgagcgtggg tctcgcgta tcattgcagc actggggcca gatggtaagc 960
cctcccgat cgtagttatc tacacgacgg ggagtcaggg aactatggat gaacgaaata 1020
gacagatcgc tgagataggt gcctcaactga ttaagcattg gtaactgtca gaccaagtt 1080
actcatatat acttagatt gattaaaac ttcatttta attaaaagg atctaggtga 1140
agatccttt tgataatctc atgacaaaaa tcccttaacg tgagtttgc ttccactgag 1200
cgtcagaccc cgtagaaaag atcaaaggat cttctgaga tccttttt ctgcgcgtaa 1260
tctgctgctt gcaaacaaaa aaaccaccgc taccagcggt ggttgtttg ccggatcaag 1320
agctaccaac tcttttccg aaggtaactg gcttcagcag agcgcagata ccaaatactg 1380
tccttctagt gtagccgtag ttaggccacc acttcaagaa ctctgttagca ccgcctacat 1440
acctcgctct gctaattctg ttaccagtgg ctgctgccag tggcgataag tcgtgtctta 1500
ccgggttggc ctcaagacga tagttaccgg ataaggcgca gcggtcgggc tgaacgggg 1560
gttcgtgcac acagcccagc ttggagcgaa cgacctacac cgaactgaga tacctacagc 1620
gtgagctatg agaaagcgcc acgcttcccg aaggggagaaa ggcggacagg tatccggtaa 1680
gcggcagggc cggaacagga gagcgcacga gggagcttcc agggggaaac gcctggatc 1740
tttatagtcc tgcgggttt cgccacctct gacttgagcg tcgattttt tgatgctcgt 1800
cagggggggc gaggctatgg aaaaacgcca gcaacgcggc cttttacgg ttccctggcct 1860
tttgctggcc tttgctcac atgttcttc ctgcgttatac ccctgattct gtggataacc 1920
gtattaccgc ctgtttagtga gctgataccg ctgcggcagc ccgaacgacc gagcgcagcg 1980
agtcaagttag gaggaaagcg gaagagcgcc caatacgcaa accgcctctc cccgcgcgtt 2040
ggccgattca ttaatgcagc tggcacgaca ggttcccgaa ctggaaagcg ggcagtgagc 2100
gcaacgcaat taatgtgagt tagctcaactc attaggcacc ccaggctta cactttatgc 2160
ttccggctcg tatgttgcgt ggaattgtga gcggataaca atttcacaca ggaaacagct 2220
atgaccatga ttacgccaag cttataatag aaatagttt ttgaaaggaa agcagcatga 2280
aaattaaaac tctggcaatc gttgttctgt cggctctgtc cctcagttct acagcggctc 2340
tggccgctgc cacgacgggtt aatggtgaaa ccgttcaatt taaaggggaa gttgttaacg 2400
ccgcttgcgc agttgatgca ggctctgttgc atcaaaccgt tcagtttagga caggttcgta 2460
ccgcattcgct ggcacaggaa ggagcaacca gttctgctgt cggtttaac attcagctga 2520
atgattgcga taccaatgtt gcatctaaag ccgcgtttgc cttttaggt acggcgattt 2580
atgcgggtca taccaacggtt ctggctctgc agagttcagc tgcgggttagc gcaacaaacg 2640
ttgggtgtgca gatcctggac agaacgggtg ctgcgtgac gctggatggc ggcacattt 2700
gttcagaaac aaccctgaat aacggaacca ataccattcc gttccaggcg cgttattttt 2760

caaccggggc cgcaaccccg ggtgctgcta atgcggatgc gaccttcaag gttcagttac	2820
aataacctac ccaggttcaag ggacgtcatt acgggcaggg atgcccaccc ttgtgcgata	2880
aaaataacga tgaaaaggaa gagattattt ctattagcgt cgttgctgcc aatgtttgt	2940
ctggccggaa ataaatggaa taccacgttgc cccggcggaa atatgaatt tcagggcgta	3000
attattgcgg aaacttgccg gattgaagcc ggtgataaac aaatgacggt caatatgggg	3060
caaatacagca gtaaccgggtt tcattgcgggtt ggggaagata ggcgcaccggt gcctttgtt	3120
attcatttac gggaaatgttag cacgggtgtt agtgaacgtg taggtgtggc gtttacgggt	3180
gtcgccggatg gtaaaaaatcc ggatgtgtt tccgtggag agggggccagg gatagccacc	3240
aatattggcg tagcggtt tgatgtgaa ggaaacctcg taccgattaa tcgtcctcca	3300
gcaaactgga aacggcttta ttcaaggctct acttcgctac atttcattcgc caaatatcgt	3360
gctaccgggc gtcgggttac tggcggcatc gccaatgccc aggctgggtt ctcttaacc	3420
tatcagtaat tggtcagcag ataatgtgat aacaggaaca ggacagttag taataaaaaac	3480
gtcaatgtaa ggaaatcgca ggaaataaca ttctgcttgc tggcaggtat cctgatgttc	3540
atggcaatga tggttgcgg acgcgctgaa gcgggagtggtt ccttaggtgc gactcgctga	3600
atttatccgg cagggcaaaa acaagagcaa ctgcggctga caaataatga tgaaaatagt	3660
acctatttaa ttcaatcatg ggtggaaaat gcccgttgc taaaggatgg tcgttttac	3720
gtgacgcctc ctctgtttgc gatgaaggaa aaaaaagaga ataccttacg tattcttgat	3780
gcaacaaata accaattgcc acaggaccgg gaaagtttac tctggatgaa cgttaaagcg	3840
atccgtcaa tggataaaatc aaaatttgact gagaatacgc tacagctcgc aattatcagc	3900
cgcattaaac tgtactatcg cccggctaaa ttgcgttgc cacccgtca ggccgcagaa	3960
aaatthaagat ttgcgtctgt cgcgaattct ctgcgttgc ttaaccgcac accctattac	4020
ctgacggtaa cagagttgaa tgccggaaacc cgggttcttgc aaaatgcatt ggtgcctcca	4080
atggcgaaa gcacggtaa attgccttct gatgcaggaa gcaatattac ttaccgaaca	4140
ataaatgatt atggcgact taccggaaa atgacggcg taatggata acgcaggggg	4200
aattttcgc ctgaataaaaa agaatttgact gcccgggtga ttttaagccg gaggaataat	4260
gtcatatctg aatthaagac ttaccagcg aaacacacaa tgcttgcata ttgcgtaaagca	4320
tcgtttggct gtttttttgc tccgactcgt tgcgttgcgttgc cacaggcacc	4380
tttgcgtatct gcccgttgcatttgcatttgc gcccgttgcgttgc cacaggcacc	4440
ggccgattta tcgcgttttgc aaaatggca agaattacccg ccagggacgt atcgctcga	4500
tatctatttgc aataatggtt atatggcaac ggcgtatgtc acatttaata cggccgacag	4560
tgaacaagggttgggatttgcgttgc ggcgtatgtc acatttaata cggccgacag	4620
ggcttctgtc gcccgtatgtc atctgctggc ggcgtatgtc tgcgttgcgttgc cacaggcacc	4680

ggtccaggac gctactgcgc atctggatgt tggtcagcag cgactgaacc tgacgatccc 4740
tcaggcattt atgagtaatc gcgcgcgtgg ttatattcct cctgagttat gggatcccgg 4800
tattaaatgcc ggattgctca attataattt cagcggaaat agtgtacaga atcggattgg 4860
gggtaacagc cattatgcat atttaaacct acagagtggg ttaaatattt gtgcgtggcg 4920
tttacgcgac aataccacct ggagttataa cagtagcgac agatcatcag gtagcaaaaa 4980
taaatggcag catatcaata cctggcttga gcgagacata ataccgttac gttccggct 5040
gacgctgggt gatggttata ctcagggcga tattttcgat ggtattaact ttcgcggcgc 5100
acaattggcc tcagatgaca atatgttacc cgatagtcaa agaggatttgc ccccggtat 5160
ccacggtatt gctcgtggta ctgcacaggt cactattaaa caaaatgggt atgacattta 5220
taatagtacg gtgccaccgg ggcctttac catcaacgtat atctatgccg caggtaatag 5280
tggtgacttg caggtAACGA tcaaagaggc tgacggcagc acgcagattt ttaccgtacc 5340
ctattcgtaa gtcccgctt tgcaacgtga agggcatact cgttattcca ttacggcagg 5400
agaataccgt agtggaaatg cgccggcagga aaaaacccgc tttttccaga gtacattact 5460
ccacggccctt ccggctggct ggacaatata tggtggaaacg caactggcgg atcggttatcg 5520
tgcttttaat ttccggatcg ggaaaaacat gggggcactg ggcgctctgt ctgtggatata 5580
gacgcaggct aattcccacac ttcccgatga cagtcagcat gacggacaat cggtgcggtt 5640
tctctataac aaatcgctca atgaatcagg cacgaatatt cagttatgg gttaccgtta 5700
ttcgaccagc ggatatttta atttcgctga tacaacatac agtcgaatga atggctacaa 5760
cattgaaaca caggacggag ttattcaggt taagccggaa ttcaccgact attacaacct 5820
cgcttataac aaacgcggga aattacaact caccgttact cagcaactcg ggcgcacatc 5880
aacactgtat ttgagtggtt gccatcaaac ttattggga acgagtaatg tcgatgagca 5940
attccaggtt ggattaaata ctgcgttcga agatataac tggacgctca gctatagcct 6000
gacggaaaaac gcctggcaaa aaggacggga tcagatgtta ggcgttaacg tcaatattcc 6060
tttcagccac tggctgcgtt ctgacagttaa atctcagtgg cgacatgcca gtgcgcgtt 6120
cagcatgtca cacgatctca acggtcggat gaccaatctg gctgggttat acggtaatcg 6180
gctggaaagac aacaacctca gctatagcgt gcaaacccgc tatgccccgg gaggcgatgg 6240
aaatagcggaa agtacaggct acgccacgct gaattatcgc ggtggttacg gcaatgccaa 6300
tatcggttac agccatagcg atgatattaa gcagctctat tacggagtca gcggtgggg 6360
actggctcat gccaatggcg taacgctggg gcagccgtt aacgatacgg tggtgcttgc 6420
taaagcgcctt ggccggcaaaatg atgcaaaatg cggaaaccag acgggggtgc gtaccgactg 6480
gcgtggttat gccgtgctgc cttatgccac tgaatatcgg gaaaatagag tggcgcttgg 6540
taccaataacc ctggctgata acgtcgattt agataacgca gttgcttaacg ttgttcccac 6600

tcgtggggcg atcgtgcgag cagagttaa agcgcgcgtt gggataaaac tgctcatgac 6660
gctgaccac aataataagc cgctgccgtt tggggcgatg gtgacatcg agagtagcca 6720
gagtagcggc attgttgcgg ataatggtca ggttacctc agcggaatgc cttagcggg 6780
aaaagttcag gtgaaaatggg gagaagagga aaatgctcac tgtgtcgcca attatcaact 6840
gccaccagag agtcagcagc agttattaac ccagctatca gctgaatgtc gttaaggggg 6900
cgtgatgaga aacaaacctt ttatcttct gtgcgtttt ttgtggctgg cggtagtca 6960
cgcttggct gcggatagca cgattactat ccgcggctat gtcaggata acggctgttag 7020
tgtggccgct gaatcaacca atttactgt tgatctgatg gaaaacgcgg cgaagcaatt 7080
taacaacatt ggcgcgacga ctccgttgc tccatttcgt atttgctgt caccctgtgg 7140
taatgccgtt tctgccgtaa aggtgggtt tactggcggt gcagatagcc acaatgcca 7200
cctgcttgcgc tttgaaaata cggtgtcagc ggcttcggga ctggaaatac agcttctgaa 7260
tgagcagcaa aatcaaatac cccttaatgc tccatcggtcc gcgcgttgcgt ggacgaccct 7320
gacgcccgggt aaaccaaata cgctgaattt ttacgcccgg ctaatggcga cacaggtgcc 7380
tgtcaactgcg gggcatatca atgccacggc taccttcaact cttgaatatac agtaactgg 7440
gatgctcatg aaatggtgca aacgtggta tgtattggcg gcaatattgg cgctcgcaag 7500
tgccgacgata caggcagccg atgtcaccat cacggtaac ggttaaggtcg tcgccaaacc 7560
gtgtacgggtt tccaccacca atgccacggc tgatctcggt gatcttatt cttcagtct 7620
tatgtctgcc gggcgccat cggcctggca tgatgtcggt cttgagttga ctaattgtcc 7680
ggtgggaacg tcgagggtca ctgccagctt cagcggggca gccgacagta ccggatatta 7740
taaaaaccag gggaccgcgc aaaacatcca gtttagagcta caggatgaca gtggcaacac 7800
attgaatact ggcccaacca aaacagttca ggtggatgat tcctcacaat cagcgcactt 7860
cccgttacag gtcagagcat tgacagtaaa tggcggagcc actcaggaa ccattcaggc 7920
agtgattagc atcacctata cctacagctg aacccgaaga gatgattgtatc atgaaacgag 7980
ttattaccct gtttgcgtta ctgctgatgg gctggcggtt aaatgcctgg tcattcgcc 8040
gtaaaaccgc caatggtacc gctatcccta ttggcggtgg cagcgccaat gtttatgtaa 8100
accttgcgc cgtcgtaat gtggggcaaa acctggcggtt ggatcttcg acgcaaatct 8160
tttgcataa cgattatccg gaaaccatta cagactatgt cacactgcaa cgaggctcg 8220
cttatggcggtt cgtgttatct aattttccg ggaccgtaaa atatagtggc agtagctatc 8280
catttcctac caccagcgaa acgcccgcgtt ttgttataa ttgcgagaacg gataagccgt 8340
ggccgggtggc gctttatttg acgcctgtga gcagtgcggg cgggggtggcg attaaagctg 8400
gctcattaaat tgccgtgctt attttgcgac agaccaacaa ctataacagc gatgatttcc 8460
agtttgcgtt gatatattac gccaataatg atgtgggtggt gcctactggc ggctgcgatg 8520

tttctgctcg tcatgtcacc gttactctgc cgactaccc tggttcagtg ccaattccctc 8580
ttaccgttta ttgtgcgaaa agccaaaacc tgggttatta cctctccggc acaaccgcag 8640
atgcgggcaa ctcgatttc accaataccg cgtcggtttc acctgcacag ggcgtcggcg 8700
tacagttgac gcgcaacggt acgattattc cagcgaataa cacggtatcg ttaggagcag 8760
tagggacttc ggcggtgagt ctgggattaa cgccaaatta tgcacgtacc ggagggcagg 8820
tgactgcagg gaatgtgcaa tcgattattg cggtgacttt tggttatcaa taatctagaa 8880
ggatccccgg gtaccgagct cgaattcact ggccgtcggt ttacaacgtc gtgactggga 8940
aaaccctggc gttacccaac ttaatcgctc tgcatcgacat ccccccggc ccagctggcg 9000
taatagcgaa gaggccccga ccgatcgccc ttcccaacag ttgcgcagcc tgaatggcga 9060
atggcgccctg atgcggtatt ttctccttac gcatctgtgc ggtatttcac accgcataatg 9120
gtgcactctc agtacaatct gctctgatgc cgcatagttt agccagcccc gacacccggc 9180
aacacccgct gacgcgcctt gacgggcttg tctgctcccg gcatccgctt acagacaagc 9240
tgtgaccgtc tccgggagct gcatgtgtca gaggtttca ccgtcatcac cgaaacgcg 9299

<210> 206
<211> 8464
<212> DNA
<213> pFIMAICDFG

<400> 206
cgagacgaaa gggcctcgat atacgcctat tttataggt taatgtcatg ataataatgg 60
tttcttagac gtcaggtggc acttttcggg gaaatgtgcg cgaaacccctt atttgtttat 120
ttttctaaat acattcaaattt atgtatccgc tcatgagaca ataaccctga taaatgcttc 180
aataatattt aaaaaggaag agtatgagta ttcaacattt ccgtgtcgcc cttattccct 240
ttttgcggc attttgcctt cctgttttgc ctcacccaga aacgctggtg aaagtaaaag 300
atgctgaaga tcagttgggt gcacgagggtt gttacatcga actggatctc aacagcggta 360
agatccttga gagtttgcgc cccgaagaac gtttccaat gatgagcact tttaaagttc 420
tgctatgtgg cgccgttattt tcccgatttgc acgccccggca agagcaactc ggtcgccgca 480
tacactattt tcagaatgac ttgggtttagt actcaccagt cacagaaaag catcttacgg 540
atggcatgac agtaagagaa ttatgcagtgc ctggcataac catgagtgtt aacactgcgg 600
ccaaacttact tctgacaacg atcggaggac cgaaggagct aaccgctttt ttgcacaaca 660
tgggggatca tgtaactcgcc tttgatcggtt gggaaaccggaa gctgaatgaa gccataccaa 720
acgacgagcgtgacaccacg atgcctgttagt caatggcaac aacggtgcgc aaactattaa 780

ctggcgaact acttactcta gcttccggc aacaattaat agactggatg gaggcggata 840
aagttgcagg accacttctg cgctcggccc ttccggctgg ctggtttatt gctgataaat 900
ctggagccgg tgagcgtggg tctcgcgta tcattgcagc actggggcca gatggtaagc 960
cctcccgat cgtagttatc tacacgacgg ggagtcaggg aactatggat gaacgaaata 1020
gacagatcgc tgagataggt gcctcactga ttaagcattg gtaactgtca gaccaagtt 1080
actcatatat acttttagatt gatttaaaac ttcatttta atttaaaagg atcttaggtga 1140
agatccttt tgataatctc atgacaaaaa tcccttaacg tgagtttcg ttccactgag 1200
cgtcagaccc cgtagaaaaag atcaaaggat cttcttgaga tcctttttt ctgcgcgtaa 1260
tctgctgctt gcaaacaaaa aaaccaccgc taccagcggt ggttgttg ccggatcaag 1320
agctaccaac tcttttccg aaggttaactg gcttcagcag agcgcagata ccaaatactg 1380
tccttctagt gtagccgtag ttaggccacc acttcaagaa ctctgttagca ccgcctacat 1440
acctcgctct gctaattctg ttaccagtgg ctgctgccag tggcgataag tcgtgtctta 1500
ccgggttsga ctcaagacga tagttaccgg ataaggcgca gcggtcgggc tgaacggggg 1560
gttcgtgcac acagcccagc ttggagcgaa cgacctacac cgaactgaga tacctacagc 1620
gtgagctatg agaaagcgcc acgcttcccg aagggagaaa ggcggacagg tatccggtaa 1680
gcggcagggt cggaacagga gagcgcacga gggagcttc agggggaaac gcctggatc 1740
tttatagtcc tgcgggtt cgccacctct gacttgagcg tcgattttt tgatgctcg 1800
cagggggcg ggcctatgg aaaaacgcca gcaacgcggc cttttacgg ttccctggcct 1860
tttgctggcc ttttgctcac atgttcttc ctgcgttatac ccctgattct gtggataacc 1920
gtattaccgc ctttgagtga gctgataccg ctgcggcagc ccgaacgacc gagcgcagcg 1980
agtcaagttag cgaggaagcg gaagagcgcc caatacgcaa accgcctctc cccgcgcgtt 2040
ggccgattca ttaatgcagc tggcacgaca ggttcccgta ctggaaagcg ggcagttagc 2100
gcaacgcaat taatgtgagt tagctcactc attaggcacc ccaggctta cactttatgc 2160
ttccggctcg tatgttgtgt ggaatttgta gcggataaca atttcacaca ggaaacagct 2220
atgaccatga ttacgccaag cttataatag aaatagttt ttgaaaggaa agcagcatga 2280
aaattaaaac tctggcaatc gttgtctgt cggctctgta cctcagttct acagcggctc 2340
tggccgctgc cacgacggtt aatggtgaaa ccgttcaatt taaaggggaa gttgttaacg 2400
ccgcttgcgc agttgatgca ggctctgtt atcaaaccgt tcagtttagga caggttcgta 2460
ccgcacatcgct ggcacaggaa ggagcaacca gttctgctgt cggtttaac attcagctga 2520
atgattgcga taccaatgtt gcatctaaag ccgctgttc ctttttaggt acggcgattg 2580
atgcgggtca taccaacggtt ctggctctgc agagttcagc tgcgggttagc gcaacaaacg 2640
ttgggtgtgca gatcctggac agaacgggtg ctgcgtgac gctggatggc ggcacattta 2700

gttcagaaac aaccctgaat aacggaacca ataccattcc gttccaggcg cgttattttg 2760
caaccggggc cgcaaccccg ggtgctgcta atgcggatgc gaccttcaag gttcagtatc 2820
aataacctac ccaggttcag ggacgtcatt acgggcaggg atgcccaccc ttgtgcgata 2880
aaaataacga tgaaaaggaa gagattattt ctattagcgt cgttgctgcc aatgtttgct 2940
ctggccggaa ataaatggaa taccacgttgc cccggcggaa atatgcaatt tcagggcgctc 3000
attattgcgg aaacttgcgg gattgaagcc ggtgataaac aaatgacggt caatatgggg 3060
caaatcagca gtaaccggtt tcatgcggtt gggaaagata ggcgcaccggc gcctttgtt 3120
attcatttac gggaatgttag cacgggtgt agtgaacgtg taggtgtggc gtttcacggc 3180
gtcgcggatg gtaaaaatcc ggatgtgctt tccgtggag agggggcagg gatagccacc 3240
aatattggcg tagcgttgtt tgatgatgaa ggaaacctcg taccgattaa tcgtcctcca 3300
gcaaactgga aacggctta ttcaggctct acttcgctac atttcatcgc caaatatcgt 3360
gctaccgggc gtcgggttac tggcggcata gccaatgccc aggccctggtt ctctttaacc 3420
tatcagtaat tgttcagcag ataatgtgat aacaggaaca ggacagttag taataaaaac 3480
gtcaatgtaa ggaaatcgca ggaaataaca ttctgcttgc tggcaggtat cctgatgttc 3540
atggcaatga tggttgcccgg acgcgctgaa gcgggagttgg ccttaggtgc gactcgctgta 3600
atttatccgg cagggcaaaa acaagagcaa ctggccgtga caaataatga tgaaaatagt 3660
acctatttaa ttcaatcatg ggtggaaaat gccgatggtg taaaggatgg tcgttttac 3720
gtgacgcctc ctctgtttgc gatgaaggaa aaaaaagaga ataccttacg tattcttgat 3780
gcaacaaata accaattgcc acaggaccgg gaaagtttat tctggatgaa cgtaaagcg 3840
attccgtcaa tggataaatac aaaattgact gagaatacgc tacagctcgc aattatcagc 3900
cgcatataac tgtactatcg cccggctaaa ttagcgttgc cacccgatca ggccgcagaa 3960
aaattaaagat ttctgtctgtag cgcaattct ctgacgctga ttaacccgac accctattac 4020
ctgacggtaa cagagttgaa tgccggacc cgggttcttgc aaaatgcatt ggtgcctcca 4080
atgggcggaaa gcacggtaa attgccttct gatgcaggaa gcaatattac ttaccgaaca 4140
ataaaatgatt atggcgcact taccccaaaa atgacggcg taatggaata acgcaggggg 4200
aatttttgcg ctgaataaaa agaattgact gccgggggtga ttttaagccg gaggaataat 4260
gtcataatctg aatttaagac tttaccagcg aaacacacaa tgcttgcata ttctgtaa 4320
tcgtttggct gtttttttgc tccgactcgt tgctgcctgt gctttgcgg cacaggcacc 4380
tttgcatct gcccacctct atttaatcc gcgccttta gcggatgatc cccaggctgt 4440
ggccgattta tcgcgttttgc aaaatggca agaattaccg ccagggacgt atcgcgtcga 4500
tatctatttgc aataatggtt atatggcaac gcgtgatgtc acatttaata cgggcgacag 4560
tgaacaagggtt attgttccct gcctgacacg cgccaaactc gccagttatgg ggctgaatac 4620

ggcttctgtc gccgttatga atctgctggc ggatgatgcc tgtgtgccat taaccacaat 4680
ggtccaggac gctactgcgc atctggatgt tggtcagcag cgactgaacc tgacgatccc 4740
tcaggcattt atgagtaatc ggcgcgtgg ttatattcct cctgagttat gggatccccc 4800
tattaatgcc ggattgctca attataattt cagcggaaat agtgtacaga atcggattgg 4860
ggtaacagc cattatgcat atttaaacct acagagtggg ttaaatattt gtgcgtggcg 4920
tttacgcgac aataccaccc ggagttataa cagtagcgac agatcatcg gtagcaaaaa 4980
taaatggcag catatcaata cctggcttga gcgagacata ataccgttac gttcccgct 5040
gacgctgggt gatggttata ctcagggcga tattttcgat ggtattaact ttgcggcgc 5100
acaattggcc tcagatgaca atatgttacc cgatagtc aa agaggattt ccccggtat 5160
ccacggattt gtcgtggta ctgcacaggt cactattaa caaaatgggt atgacattt 5220
taatagtacg gtgcacccgg ggcctttac catcaacgtat atctatgcc caggtaatag 5280
tggtgacttg cagtaacga tcaaagaggg tgacggcagc acgcagattt ttaccgtacc 5340
ctattcgta gtcccgctt tgcaacgtga agggcatact cgttattcca ttacggcagg 5400
agaataccgt agtggaaatg cgacgcagga aaaaacccgc ttttccaga gtacattact 5460
ccacggcctt ccggctggct ggacaatata tggtggaaacg caactggcgg atcggtatcg 5520
tgctttat ttccgtatcg ggaaaaacat gggggcactg ggcgtctgt ctgtggatat 5580
gacgcaggct aattccacac ttcccgatga cagtcagcat gacggacaat cggtgcgtt 5640
tctctataac aaatcgctca atgaatcagg cacgaatatt cagttatgg gttaccgtt 5700
ttcgaccagc ggatattta atttcgctga tacaacatac agtcgaatga atggctacaa 5760
cattgaaaca caggacggag ttattcaggt taagccgaaa ttcaccgact attacaaccc 5820
cgcttataac aaacgcggga aattacaact caccgttact cagcaactcg ggcgcacatc 5880
aacactgtat ttgagtggtt gccatcaaac ttattggga acgagtaatg tcgatgagca 5940
attccaggct ggattaaata ctgcgttcga agatataac tggacgctca gctatagcct 6000
gacggaaaac gcctggcaaa aaggacggga tcagatgtt ggcgttaacg tcaatattcc 6060
tttcagccac tggctgcgtt ctgacagtaa atctcagtgg cgacatgcca gtgcgttac 6120
cagcatgtca cacgatctca acggtcggat gaccaatctg gctgggttat acggtaacgtt 6180
gctggaaagac aacaacctca gctatagcgt gcaaaaccggc tatgccggg gaggcgatgg 6240
aaatagcgga agtacaggct acgccacgct gaattatcgc ggtggttacg gcaatgcca 6300
tatcggttac agccatagcg atgatattaa gcagcttat tacggagtca gcggtgggtt 6360
actggctcat gccaatggcg taacgctggg gcagccgtt aacgatacgg tggtgcttgc 6420
taaagcgccct ggcgcaaaag atgcaaaagt cgaaaaccag acgggggtgc gtaccgactg 6480
gcgtggttat gccgtgctgc cttatgccac tgaatatcgg gaaaatagag tggcgctgga 6540

taccaataacc ctggctgata acgtcgattt agataacgcg gttgctaacg ttgttcccac 6600
tcgtggggcg atcgtgcgag cagagttaa agcgcgctt gggataaaac tgctcatgac 6660
gctgaccac aataataagc cgctgccgtt tggggcgatg gtgacatcg agagtagcga 6720
gagtagcggc attgttgcgg ataatggtca gtttacctc agcggaatgc ctttagcggg 6780
aaaagttcag gtgaaatggg gagaagagga aaatgctcac tgtgtcgcca attatcaact 6840
gccaccagag agtcagcgcg agttattaac ccagctatca gctgaatgtc gttaaggggg 6900
cgtatgaga aacaaacctt ttatcttct gtgcgtttt ttgtggctgg cggtgagtca 6960
cgcttggct gcggatagca cgattactat ccgcggctat gtcaggata acggctgttag 7020
tgtggccgct gaatcaacca atttactgt tgatctgatg gaaaacgcgg cgaagcaatt 7080
taacaacatt ggccgacga ctccgttgt tccatttcgt atttgctgt caccctgtgg 7140
taatgccgtt tctgccgtaa aggttgggtt tactggcggt gcagatagcc acaatgcaa 7200
cctgcttgcg cttgaaaata cggtgtcagc ggcttcggga ctggaaatac agcttctgaa 7260
tgagcagcaa aatcaaatac cccttaatgc tccatcgatcc ggccttcgt ggacgaccct 7320
gacgcccgggt aaaccaaata cgctgaattt ttacgcccgg ctaatggcga cacaggtgcc 7380
tgtcaactgcg gggcatatca atgccacggc taccttcaact cttgaatatc agtaactgga 7440
gatgctcatg aaatggtgca aacgtggta tgtattggcg gcaatattgg cgctcgcaag 7500
tgcgacgata caggcagccg atgtcaccat cacggtaac ggtaaggtcg tcgccaaacc 7560
gtgtacgggtt tccaccacca atgccacggt tgatctcgatc gatcttatt ctttcagtct 7620
tatgtctgcc gggcgccat cggcctggca tgatgttgcg cttgagttga ctaattgtcc 7680
ggtgggaacg tcgagggtca ctgccagctt cagcggggca gccgacagta ccggatatta 7740
taaaaaccag gggaccgcgc aaaacatcca gttagagcta caggatgaca gtggcaacac 7800
attgaatact ggccaaacca aaacagttca ggtggatgtat tcctcacaat cagcgcactt 7860
cccgttacag gtcagagcat tgacagtaaa tggcggagcc actcaggaa ccattcaggc 7920
agtgattagc atcacctata cctacagctg aacccgaaga gatgattgtat atgaaacgag 7980
ttattaccct gtttgctgtat ctgctgatgg gctggcggtt aaatgcctgg tcattcgct 8040
gtaaaaccgc caatggtacc gagctcgaat tcactggccg tcgtttaca acgtcgatc 8100
tggaaaaacc ctggcggtac ccaacttaat cgccttgcag cacatcccccc ttgcggcagc 8160
tggcgtaata gcgaagaggc cgcacccgt cgccttccc aacagttgcg cagcctgaat 8220
ggcgaatggc gcctgatgcg gtatcccttc cttacgcatac tgtgcggat ttcacaccgc 8280
atatggtgca ctctcagtac aatctgctct gatgccgat agttaagcca gccccgacac 8340
ccgccaacac cgcgtgacgc gccctgacgg gcttgcgtc tcccgccatc cgcttacaga 8400
caagctgtga cgcgtccgg gagctgcatac tgctcagaggt tttcaccgtc atcaccgaaa 8460

cgcg

8464

<210> 207
<211> 13
<212> PRT
<213> Ce3epitope

<400> 207
Cys Gly Gly Val Asn Leu Thr Trp Ser Arg Ala Ser Gly
1 5 10

<210> 208
<211> 13
<212> PRT
<213> Ce3mimotope

<400> 208
Cys Gly Gly Val Asn Leu Pro Trp Ser Phe Gly Leu Glu
1 5 10

<210> 209
<211> 9
<212> PRT
<213> Bee venom phospholipase A2 cloning vector

<400> 209
Ala Ala Ala Ser Gly Gly Cys Gly Gly
1 5

<210> 210
<211> 145
<212> PRT
<213> PLA₂ fusion protein

<400> 210
Met Ala Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys
1 5 10 15

Ser Ser Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys
20 25 30

Cys Arg Thr Gln Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser
35 40 45

Lys His Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp
50 55 60

Cys Asp Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile
65 70 75 80

Ser Ser Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys
85 90 95

Cys Tyr Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu
100 105 110

Gly Arg Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr
115 120 125

Gln Trp Phe Asp Leu Arg Lys Tyr Ala Ala Ser Gly Gly Cys Gly
130 135 140

Gly
145

<210> 211
<211> 17
<212> PRT
<213> Ce4mimotope

<400> 211
Gly Glu Phe Cys Ile Asn His Arg Gly Tyr Trp Val Cys Gly Asp Pro
1 5 10 15

Ala

<210> 212
<211> 27
<212> PRT
<213> Synthetic M2 Peptide

<400> 212
Ser Leu Leu Thr Glu Val Glu Thr Pro Ile Arg Asn Glu Trp Gly Cys
1 5 10 15
Arg Cys Asn Gly Ser Ser Asp Gly Gly Cys
20 25

<210> 213
<211> 97
<212> PRT
<213> Matrix protein M2

<400> 213
Met Ser Leu Leu Thr Glu Val Glu Thr Pro Ile Arg Asn Glu Trp Gly
1 5 10 15
Cys Arg Cys Asn Gly Ser Ser Asp Pro Leu Ala Ile Ala Ala Asn Ile
20 25 30
Ile Gly Ile Leu His Leu Ile Leu Trp Ile Leu Asp Arg Leu Phe Phe
35 40 45
Lys Cys Ile Tyr Arg Arg Phe Lys Tyr Gly Leu Lys Gly Gly Pro Ser
50 55 60

Thr Glu Gly Val Pro Lys Ser Met Arg Glu Glu Tyr Arg Lys Glu Gln
65 70 75 80
Gln Ser Ala Val Asp Ala Asp Asp Gly His Phe Val Ser Ile Glu Leu
85 90 95

Glu

<210> 214
<211> 42
<212> DNA

<213> Oligonucleotide

<400> 214
taaccgaatt caggaggtaa aaacatatgg ctatcatctaa cc 42

<210> 215

<211> 129
<212> PRT

<213> Bacteriophage f2

<400> 215

Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asn Asp Gly Gly Thr Gly
1 5 10 15

Asn Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp
20 25 30

Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val
35 40 45

Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val
50 55 60

Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val Ala
65 70 75 80

Ala Trp Arg Ser Tyr Leu Asn Leu Glu Leu Thr Ile Pro Ile Phe Ala
85 90 95

Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu
100 105 110

Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile
115 120 125

Tyr

<210> 216

<211> 17

<212> PRT

<213> Circular Mimotope

<400> 216

Gly Glu Phe Cys Ile Asn His Arg Gly Tyr Trp Val Cys Gly Asp Pro
1 5 10 15

Ala

<210> 217

<211> 329

<212> PRT

<213> Bacteriophage Q-beta

<400> 217

Met Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly
1 5 10 15

Lys Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly
20 25 30

Val Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
35 40 45

Val Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
50 55 60

Val Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser
65 70 75 80

Cys Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser
85 90 95

Phe Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu
100 105 110

Leu Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln
115 120 125

Leu Asn Pro Ala Tyr Trp Thr Leu Leu Ile Ala Gly Gly Ser Gly
130 135 140

Ser Lys Pro Asp Pro Val Ile Pro Asp Pro Pro Ile Asp Pro Pro Pro
145 150 155 160

Gly Thr Gly Lys Tyr Thr Cys Pro Phe Ala Ile Trp Ser Leu Glu Glu
165 170 175

Val Tyr Glu Pro Pro Thr Lys Asn Arg Pro Trp Pro Ile Tyr Asn Ala
180 185 190

Val Glu Leu Gln Pro Arg Glu Phe Asp Val Ala Leu Lys Asp Leu Leu
195 200 205

Gly Asn Thr Lys Trp Arg Asp Trp Asp Ser Arg Leu Ser Tyr Thr Thr
210 215 220

Phe Arg Gly Cys Arg Gly Asn Gly Tyr Ile Asp Leu Asp Ala Thr Tyr
225 230 235 240

Leu Ala Thr Asp Gln Ala Met Arg Asp Gln Lys Tyr Asp Ile Arg Glu
245 250 255

Gly Lys Lys Pro Gly Ala Phe Gly Asn Ile Glu Arg Phe Ile Tyr Leu
260 265 270

BACTERIOPHAGE Q-BETA

Lys Ser Ile Asn Ala Tyr Cys Ser Leu Ser Asp Ile Ala Ala Tyr His
275 280 285

Ala Asp Gly Val Ile Val Gly Phe Trp Arg Asp Pro Ser Ser Gly Gly
290 295 300

Ala Ile Pro Phe Asp Phe Thr Lys Phe Asp Lys Thr Lys Cys Pro Ile
305 310 315 320

Gln Ala Val Ile Val Val Pro Arg Ala
325

<210> 218

<211> 770

<212> PRT

<213> Amyloid-Beta Protein (Homo Sapiens)

<400> 218

Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg
1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala
355 360 365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp
370 375 380

Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
385 390 395 400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
405 410 415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
420 425 430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
435 440 445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
450 455 460

Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
465 470 475 480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
500 505 510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Val Glu Leu Leu Pro
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705 710 715 720

Val Met Leu Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
755 760 765

Gln Asn
770

<210> 219

<211> 82

<212> PRT

<213> Beta-Amyloid Peptide Precursor (Homo Sapiens)

<400> 219

Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys
1 5 10 15

Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln
20 25 30

Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile
35 40 45

Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Ile Ile
50 55 60

Thr Leu Val Met Leu Lys Lys Gln Tyr Thr Ser Asn His His Gly Val
65 70 75 80

Val Glu

<210> 220

<211> 42

<212> PRT

<213> Amyloid Beta Peptide

<400> 220

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala
35 40

221:

RANKL_human: TrEMBL:O14788: extracellular domain

YFRAQMDPNRIS EDGTHCIYRI LRLHENADFQ DTTLESQDTK LIPDSCRRRIK QAFQGAVQKE
LQHIVGSQHI RAEKAMVDGS WLDLAKRSKL EAQPF AHLTI NATDIPSGSH KVSLSSWYHD
RGWAKISNMT FSNGKLIVNQ DGFYYLYANI CFRHHETSGD LATEYLQLMV YVTKTSIKIP
SSHTLMKGGS TKYWSGNSEF HFYSINVGGF FKLRSGEEIS IEVSNPSLLD PDQDATYFGA FKVRDID

222:

RANKL_human: spliced isoformTrEMBL:O14788

MDPNRISEDG THCIYRILRL HENADFQDTT LESQDTKLIP DSCRRRIKQAF QGAVQKELQH
IVGSQHRAE KAMVDGSWLD LAKRSKLEAQ PFAHLTINAT DIPSGSHKVS LSSWYHDRGW
AKISNMTFSN GKLIVNQDG YYLYANICFR HHETSGDLAT EYLQLMVYVT KTSIKIPSSH
TLMKGGSTKY WSGNSEFHFY SINVGGFFKL RSGEEISIEV SNPSLLDPDQ DATYFGAFKV
RDID

223:

RANKL_mouse: TrEMBL:O35235: extracellular domain

YFRAQMDPNRI SEDSTHCFYR ILRLHENAGL QDSTLESEDT LPDSCRRMKQ AFQGAVQKEL
QHIVGPQRFS GAPAMMEGSW LDVAQRGKPE AQPF AHLTIN AASIPSGSHK VTLSSWYHDR

GWAKISNMTL SNGKLRVNQD GFYYLYANIC FRHETSGSV PTDYLQLMVY VVKTSIKIPS
SHNLMKGGST KNWSGNSEFH FYSINVGGFF KLRALEEISI QVSNPSLLDP DQDATYFGAF KVQDID

224:

RANKL_mouse spliced isoforms: TrEMBL:Q9JJK8

MKQAFQGAVQ KELQHIVGPQ RFSGAPAMME GSWLDVAQRG KPEAQPF AHL TINAASIPSG
SHKVTLSSWY HDRGWAKISN MTLSNGKLRV NQDGFYLYA NICFRHETS GSVPTDYLQL
MVYVVKTSIK IPSSHNLMKG GSTKNWSGNS EFHFYSINVG GFFKLRALEE ISIQVSNPSL
LDPDQDATYF GAFKVQDID

225:

MIF_rat: SwissProt

PMFIVNTNVP RASVPEGFLS ELTQQLAQAT GKPAQYIAVH VVPDQLMTFS GTSDPCALCS
LHSIGKIGGA QNRNYSKLLC GLLSDRLHIS PDRVYINYD MNAANVGWNG STFA

226:

MIF_mouse: SwissProt

PMFIVNTNVP RASVPEGFLS ELTQQLAQAT GKPAQYIAVH VVPDQLMTFS GTNDPCALCS
LHSIGKIGGA QNRNYSKLLC GLLSDRLHIS PDRVYINYD MNAANVGWNG STFA

227:

MIF_human: SwissProt

PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRYSKLLC GLLAERLRIS PDRVYINYD MNAANVGWNN STFA

228:

Human IL-17

ACCESSION #: AAC50341

1 mtpgktslvs lllllsleai vkagitiprn pgcpnsedkn fprtvmvnln ihnrrntntnp
61 krssdyynrs tspwnlhrne dperypsvi eakcrhlgci nadgnvdyhm nsvpiqqeil
121 vlrrepphcp nsfrlekilv svgctcvtpi vhhva

229:

Mouse IL-17

ACCESSION #: AAA37490

1 mspgrassvs lmllllsla atvkaaaiip qssacpntea kdflqnvkvn lkfnslgak
61 vssrrpsdyl nrstspwtlh rnedpdryps viweaqcrhq rcvnaegkld hhmnsvliqq
121 eilvlkrepe scpftrvek mlvgvgctcv asivrqaa

230:

Human IL-13 (precursor)

MALLTTVIALTCLGGFASPGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSG
CSAIEKTQRLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKKLFREGRFN

231:
Human IL-13 (processed)

GPVPPSTALR ELIEELVNIT QNQKAPLCNG SMVWSINLTA
GMYCAALESL INVSGCSAIE KTQRLSGFC PHKVSAGQFS SLHVRDTKIE VAQFVKDLLL
HLKKLFREGR FN

232:
Mouse IL-13 (processed)

GPVPRSVSLPLTLKELIEELSNITQDQTPLCNGSMVWSVDLAAGGFCVALDSL TNISNCNAIYRTQRILHGLCNR
KAPTTVSSL PDTKIEVAHFITKLLSYTKQLFRHGPF

233:
Human IL-5 (precursor)

MRMLLHLSLL ALGAAYVYAI PTEIPTSLV KETLALLSTH RTLLIANETL RIPVPVHKNH
QLCTEEIFQG IGTLESQTVQ GGTVERLFKN LSLIKKYIDG QKKKCGEERR RVNQFLDYLQEFLGVMNTIEW
IIES

234:
Human IL-5 (processed)

I PTEIPTSLV KETLALLSTH RTLLIANETL RIPVPVHKNH
QLCTEEIFQG IGTLESQTVQ GGTVERLFKN LSLIKKYIDG QKKKCGEERR RVNQFLDYLQ
EFLGVMNTIEW IIES

235:
Mouse IL-5 (processed)

MEIPMSTVVKETLTQLSAHRALLTSNETMRLPVPTHKNHQLCIGEIFQQLDILKNQTVRGGTVEMLFQNLSLIKK
YIDRQKEKCGEERRRTRQFLDYLQEFLGVMSTEWAMEG

236:
CCL21 Swissprot: SY21_human: Sequence after cleavage of signal peptide:
SDGGAQD CCLKYSQRKI PAKVVRSYRK QEPSLGCSIP AILFLPRKRS QAEELCADPKE LWVQQLMQHL
DKTPSPQKPA QGCRKDRGAS KTGKKKGSK GCKRTERSQT PKGP

237:
CCL21 Swissprot: SY21_mouse: Sequence after cleavage of signal peptide:
SDGGGQD CCLKYSQKKI PYSTVRGYRK QEPSLGCPIP AILFSPRKHS KPELCANPEE GWVQNLMRRL

DQPPAPGKQS PGCRKNRGT S KSGKKKGSK GCKRTEQTQP SRG

238:

Swissprot: SDF1_human: Sequence after cleavage of signal peptide:

DGKPVSLSYRC PCRFFESHVA RANVKHLKIL NTPNCALQIV ARLKNNNRQV CIDPKLKWIQ
EYLEKALNKR FKM

239:

Swissprot: SDF1_mouse: Sequence after cleavage of signal peptide:

DGKPVSLSYRC PCRFFESHIA RANVKHLKIL NTPNCALQIV ARLKNNNRQV CIDPKLKWIQ
EYLEKALNPK

240:

BLC Sequences: Human: Accession: NP_006410

Amino acids 1-22 are signal peptide.

MKFISTSLLL MLLVSSLSPV QGVLEVYYTS LRCRCVQESS VFIPRRFIDR IQILPRGNNGC
PRKEIIIVWKK NKSIVCVDPQ AEWIQRMMEV LRKRSSSTLP VPVFKRKIP

241:

BLC Sequence Mouse: accession: NP_061354

Amino acids 1-21 are signal peptide

MRLSTATLLL LLASCLSPGH GILEAHYTNL KCRCSGVIST VVGLNIIDRI QVTPPGNGCP
KTEVVIWTKM KKVICVNPR A KWLQRLLRH V QSKSLSSTPQ APVSKRRAA

242:

Human Eotaxin-1

1-23 is Signal peptide

1 mkvsallwl lliaaafspq glagpasvpt tccfnlanrk iplqrlesyr ritsgkcpqk
61 avifktklak dicadpkkkw vqdsmkyldq ksptpkp

243:

Human Eotaxin-2

1-26 is Signal peptide

1 maglmtivts llflgvcahh iiptgsvvip spccmffvsk ripenrvvssy qlssrstclk
61 agvifttkkg qqfcgdpkqe wvqrymknld akqkkaspra ravavkgpvq rypgnqttc

244:

Human Eotaxin-3

1-23 is signal peptide

1 mmglslasav llasllslhl gtatrgsdis ktccfqyshk plpwtwvrsy eftsnscsqr
61 avifttkrgk kvcthprkkw vqkyisllkt pkql

245:

Mouse Eotaxin-1

1-23 is signal peptide

1 mqsstallfl lltvtsftsq vlahpgsipt sccfimtskk ipntllksyk ritnnrctlk
61 aivfktrlgk eicadpkkkw vqdatkhldq klqtpkp

246:

Mouse Eotaxin-2

1-25 is signal peptide

1 magsativag llllvacacc ifpidsvtip sscctsfisk kipenrvvsvy qlangsicpk
61 agvifitkgk hkictdpkll wvqrhiqkld akknqpskga kavrtrkfavq rrrgnstev

247:

M-CSF Sequence: human: the construct would be an N-terminal fragment consisting of residue 33 -181 or 33 –185, corresponding to the soluble form of the receptor.

Accession: NP_000748

MTAPGAAGRC PPTTWLGSLL LLVCLLASRS ITEEVSEYCS HMIGSGHLQS LQRLIDSQME
TSCQITFEFV DQEQLKDPVC YLKKAFLLVQ DIMEDTMRFR DNTPNAIAIV QLQELSLRLK
SCFTKDYEEH DKACVRTFYE TPLQLLEVKV NVFNETKNLL DKDWNIFSKN CNNSFAECSS
QDVVTKPDCN CLYPKAIPSS DPASVSPHQD LAPSMAPVAG LTWEDSEGTE GSSLLPGEQP
LHTVDPGSAK QRPPRSTCQS FEPPETPVVK DSTIGGSPQP RPSVGAFNPG MEDILDSAMG
TNWVPEEASG EASEIIPVPGQ TELSPSPRPGG GSMQTEPARP SNFLSASSPL PASAKGQQPA
DVTGTALPRV GPVRPTGQDW NHTPQKTDHP SALLRDPPEP GSPIRSSPRP QGLSNPSTLS
AQPQLSRSHS SGSVLPLGEL EGRRSTRDRR SPAEPEGGPA SEGAARPLPR FNSVPLTDTH
ERQSEGSSSSP QLQESVFHLL VPSVILVLLA VGGLLFYRWR RRSHQEPRQA DSPLEQPEGS
PLTQDDRQVE LPV

248:

M-CSF Mouse sequence: Mature sequence starts at amino acid 33. Accession. NP_031804

MTARGAAGRC PSSTWLGSRL LLVCLLMSRS IAKEVSEHCS HMIGNGHLKV LQQLIDSQME
TSCQIAFEFV DQEQLDDPVC YLKKAFFLVQ DIIDETMRFK DNTPNANATE RLQELSNNLN
SCFTKDYEEQ NKACVRTFHE TPLQLLEKIK NFFNETKNLL EKDWNIFTKN CNNSFAKCSS
RDVVTKPDCN CLYPKATPSS DPASASPHQD PAPSMAPLAG LAWDDDSQRTE GSSLLPSELP
LRIEDPGSAK QRPPRSTCQT LESTEQPNHG DRLTEDSQPH PSAGGPVPGV EDILESSLGT
NWVLEEASGE ASEGFQLEA KFSPSTPVGG SIQAETDRPR ALSASPFPKS TEDQKPVDT

DRPLTEVNPM RPIGQTQNNT PEKTDGTSTL REDHQEPGSP HIATPNPQRV SNSATPVAQL
LLPKSHSWGI VLPLGELEGK RSTRDRRSPA ELEGGSASEG AARPVARFNS IPLTDTGHVE
QHEGSSDPQI PESVFHLLVP GIILVLLTVG GLLFYKWKWR SHRDPQTLDS SVGRPEDSSL
TQDEDRQVEL PV

249:

Sequence of Human Resistin: Precursor.

MKALCLLLLVLGLLVSSKTLCSMEEAINERIQEVAGSLIFRAISSIGLEQS VTSRGDLATCPRGF AVTGCTCG
SACGSWDVRAETTCHCQCAGMDWTGARCCRVQP

250:

Sequence of Mouse Resistin: Precursor.

MKNLSFPLLFLFFLVPELLGSSMPLCPIDEAIDKKIKQDFNSLF PNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSC
GSACGSWDIREEKVCHCQCARI DWTAARCKLQVAS

251:

Lymphotoxin- β :

Swissprot: TNFC_human: Sequence of the extracellular domain:

QD QGGLVTETAD PGAQAQQGLG FQKLPEEEPE TDLS PGLPAA HLIGAPLKGQ GLGWETTKEQ
AFLTSGTQFS DAEGLALPQD GLYYLYCLVG YRGRAPPGGG DPQGRSVTLR SSLYRAGGAY GPGTPELLLE
GAETVTPVLD PARRQGYGPL WYTSVGFGL VQLRRGERVY VN

252:

Lymphotoxin- β :

Swissprot: TNFC_mouse: Sequence of the extracellular domain:

QD QGRRVEKIIIG SGAQAQKRLD DSKPSCILPS PSSLSETPDP RLHPQRSNAS RNLASTSQGP
VAQSSREASA WMTILSPAAD STPDPGVQQL PKGEPETDLN PELPAAHЛИ AWMSGQGLSW
EASQEEAFLR SGAQFSPTHG LALPQDGVYY LYCHVGYRGR TPPAGRSRAR SLTLRSALYR
AGGAYGRGSP ELLLEGAETV TPVVDPIGYG SLWYTSVGFGL GLAQLRSGER VYVNISHPDM
VDYRRGKTF GAVMVG

253:

RNA-phage PP7:

msktivlsvg eatrtlteiq stadrqifee kvgplvgrlr ltaslrqnga ktayrvnkl
dqadadvdcst svcgelpkvr ytqvwshdvt ivansteasr kslydlksl vatsqvedlv
vnlvplgr

254:

RNA-phage SP A1 protein:

aklnqvts kigkngdqt1 tltprgvnpt ngvaslseaag avpalekrvt vsvaqpsrnr
knfkvqiklq nptactrdac dpsvtrsafa dvtlsftsys tdeeralirt elaalladpl
ivdaihdlnp awaallvas sgggdnpdsvp pdgtgrykcp facyrlgsiy
evgkegspdi yergdevsvt fdyaledflg ntnwrnwdqr lsdydianrr rcrgngyidl
datamqsddf vlsgrgvrk vkfpgafgsi kyllniqgda wldlsevtay rsygmwigfw
tdskspqlpt dftqfnnsanc pvqtviiips 1

255:

“QB 240”:

AKLETVLGNIGRDGKQTLVNPGRVNPTNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSFTQYSTDEERAFAVRTELAALLASPLLIDAIDQLNPAY

256:

“QB 243”:

AKLETVTLGKIGKDGKQTLVNPQGVNPNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSFTQYSTDEERAFAVRTELAALLASPLLIDAIDQLNPAY

257:

“QB 250”:

**ARLETVTLGNIGRDGKQLVLNPRGVNPNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTF SFTQYSTDEERA FVRTEL AALLASPLLIDAIDQLNPAY**

258:

“Qβ 259”:

ARLETVTLGNIGKDGRQLVLPNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSVPQRNRKKNVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSTOYSTDEERAFVRTELALLASPLLIDAIDQLNPAY

259:

“QB 251”:

AKLETVTLGNIGKDGRQTLVLPNGVNASLSQAGAVP
ALEKRVTVSVPNSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSFTOYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

260:

PH19 (SEQ ID NO:260)

TAAGTCCTCTGCCACGTACC

261:

PH20 (SEQ ID NO:261)

TGGAAACCACGCTCACTTCC

262:

PH21 (SEQ ID NO:262)

CGGGATCCGGGATGAAGAACCTTCATTC

263:

PH22 (SEQ ID NO:263)

GCCTCTAGAGAGGAAGCGACCTGCAGCTTAC

264:

PH29 (SEQ ID NO:264)

CTAGGGGGAGGGGGTGGATGTGGGGACGACTACAAGGATGACCGACA

265:

PH30 (SEQ ID NO:265)

AGCTTGTCTCATCCTTGTAGTCGTCCCCACATCCACCCCTCCCG

266:

PH31 (SEQ ID NO:266)

AGCTTACTCACACATGCCCAACCGTGCCAGCACCTGAAGCCGAGG

267:

PH32 (SEQ ID NO:267)

CGGCTTCAGGTGCTGGGCACGGTGGGCATGTGTGAGTA

268:

PH35 (SEQ ID NO:268)

CTAGCGGGAGGGGGTGGATGTGGGATCGAAGGTCGCA

269:

PH36 (SEQ ID NO:269)

AGCTTGCGACCTCGATCCCACATCCACCCCTCCG

270:

PH37 (SEQ ID NO:270)

CGGGATCCAGCAGCTGGGCTCGAGGTGCTAGCTTGTAAAC

271:

PH38 (SEQ ID NO:271)

GATCGTTAACAAACAAAGCTAGCACCTCGAGCCCAGCTGGATCCGGTAC

272:

PH39 (SEQ ID NO:272)

CTAGCGGGAGGGGGTGGATGTGGGACGATGACGACA

273:

PH40 (SEQ ID NO:273)

AGCTTGTGTCATCGTCCCCACATCCACCCCTCCG

274:

PH41 (SEQ ID NO:274)

CATGGAGACAGACACACTCCTGCTATGGGT

275:

PH42 (SEQ ID NO:275)

GCAGTACCCATAGCAGGAGTGTGTCTGTCTCCATGGTAC

276:

PH43 (SEQ ID NO:276)

ACTGCTGCTCTGGTTCCAGGTTCCACTGGTGACGCG

277:

PH44 (SEQ ID NO:277)

GATCCGCGTCACCACTGGAACCTGGAACCCAGAGCA

1005091234567890

278:

SU7 (SEQ ID NO:278)

AGCTTGGGATCCAGGATATCGGCTCGAGGTTCTAGAGTG

279:

SU8 (SEQ ID NO:279)

GGCCCACCTCTAGAACCTCGAGCCGATATCCTGGATCCGCA

280:

Resistin-C-Xa:

SSMPLCPIDEAIKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG
SACGSWDIREEKVCHCQCARIWTAARCKLQVASSLAGGGCGIEGR

281:

Resistin-C-EK

SSMPLCPIDEAIKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG
SACGSWDIREEKVCHCQCARIWTAARCKLQVASSLAGGGCGDDDD

282:

Resistin-GCG:

SSMPLCPIDEAIKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG
SACGSWDIREEKVCHCQCARIWTAARCKLQVASSLAGGGCG

283:

pCep-Xa-Fc*: (complete sequence)

1 GCCCGCCGC CGGACGAAC TAAACCTGACT ACGGCATCTC TGCCCCTTCT TCGCTGGTAC GAGGAGCGCT
71 TTTGTGTTGT ATTGGGGCA GTGCATGAA TCCCTCTAGT TGGTTGGTAC AACTTGCCAA CTGGGCCCTG
141 TTCCACATGT GACACGGGGG GGGACCAAAC ACAAAAGGGT TCTCTGACTG TAGTTGACAT CCTTATAAAT
211 GGATGTGCAC ATTGCGAAC ACTGAGTGGC TTTCATCTG GAGCAGACTT TGCATGCTGT GGACTGCAAC
281 AACACATTGC CTTTATGTGT AACTCTTGGC TGAAGCTTT ACACCAATGC TGGGGGACAT GTACCTCCA
351 GGGGCCCAAG AAGACTACGG GAGGCTACAC CAACGTCAAT CAGAGGGGCC TGTGTAGCTA CCGATAAGCG
421 GACCTCAAG AGGCATTAG CAATACTGTT TATAAGGCC CCTTGTAAAC CCTAACAGGG TAGCATATGC
491 TTCCGGGTA GTAGTATATA CTATCCAGAC TAACCTTAAT TCAATAGCAT ATGTTACCCA ACGGGAAAGCA
561 TATGCTATCG AATTAGGGT AGTAAAGGG TCCTAAGGA CAGCGATATC TCCCAACCCA TGAGCTGCA
631 CGGTTTATT TACATGGGGT CAGGATTCCA CGAGGGTAGT GAACCATTAA AGTCACAAGG GCAGTGGCTG
701 AAGATCAAGG AGCGGGCAGT GAACTCTCCT GAATCTTCG CTGCTTCTTC ATTCTCCTTC GTTTAGCTAA
771 TAGAATAACT GCTGAGTTGT GAACAGTAAG GTGTTATGTA GGTGCTCGAA AACAAGGTTT CAGGTGACGC
841 CCCCGAAATA AAATGGGAC GGGGGGTTCA GTGGTGGCAT TGTGCTATGA CACCAATATA ACCCTCACAA
911 ACCCCTGGG CAATAAATAC TAGTGTAGGA ATGAAACATT CTGAATATCT TTAACAATAG AAATCCATGG
981 GGTGGGGACA AGCGTAAAG ACTGGATGTC CATCTCACAC GAATTATGG CTATGGGCAA CACATAATCC
1051 TAGTGCATAA ACTTGTGTT GTTATTAAAGA TGTGCTCCAG GCAGGGGACCA AGACAGGTGA ACCATGTGTT
1121 TACACTCTAT TTGTAAACAG GGGAAAGAGA GTGGACGCCG ACAGCAGCGG ACTCCTACTGG TTGTCCTAA
1191 CACCCCGAA AATTAAACGG GGCTCCACGC CAATGGGCC CATAAACAAA GACAAGTGGC CACTTTTT
1261 TTGAAATTG TGGAGTGGGG GCACGCGTCA GCCCCCACAC GCGCCCTGC GGTTTTGGAC TGAAAATAA
1331 GGGTGTAATA ACTTGGCTGA TTGTAAACCC GCTAAACACT GCGGTCACAC CACTTGCAC CAAACCAACT
1401 AATGGCACCC CGGGGAAATAC CTGCGATAAG AGGTGGGCGG GCAGAGATAG GGGCGGATT GCTGCGATCT
1471 GGAGGACAAA TTACACACAC TTGCGCTGA GCGCCAAGCA CAGGGTTGTT GGTCTCATA TTCACGAGGT
1541 CGCTGAGAGC ACGGTGGGCT AATGTTGCCA TGGGTAGCAT ATACTACCA AATACTGGA TAGCATATGC
1611 TATCTTAATC TATATCTGGG TAGCATAGC TATCCTAATC TATATCTGGG TAGCATAGGC TATCCTAATC
1681 TATATCTGGG TAGTATATGC TATCCTAATC TATATCTGGG TAGTATATGC TATCCTAATC TATATCTGGG
1751 TAGCATATGC TATCCTAATC TATATCTGGG TAGTATATGC TATCCTAATT TATATCTGGG TAGCATATAC
1821 TATCCTAATA GAGATTAGGG TAGTATATGC TATCCTAATT TATATCTGGG TAGCATATAC TACCCAAATA
1891 TCTGGATAGC ATATGCTATC CTAATCTATA TCTGGGTAGC ATATGCTATC CTAATCTATA TCTGGGTAGC
1961 ATAGGCTATC CTAATCTATA TCTGGGTAGC ATATGCTATC CTAATCTATA TCTGGGTAGT ATATGCTATC
2031 CTAATTTATA TCTGGGTAGC ATAGGCTATC CTAATCTATA TCTGGGTAGC ATATGCTATC CTAATCTATA
2101 TCTGGGTAGT ATATGCTATC CTAATCTGT TCCGGGTAGC ATATGCTATC CTCATGCATA TACAGTCAGC
2171 ATATGATACC CAGTAGTAGA GTGGGAGTGC TATCCTTGC ATATGCCGC ACCTCCCAAG GGGCGTGA
2241 TTTCGCTGC TTGTCCTTT CTCGATGCT GTGGTCTCCC ATTCTTAGGT GAATTAAAGG AGGCCAGGGCT
2311 AAAGCGCTG CATGTCATG TGCTCACAG GTAAATGTC CTAATCTTT TCTGGGTAGT ATATGCTATC
2381 GGCGGAGCT GAGTGACGTG ACAACATGGG TATGCCAAT TGGCCCATGT TGGGAGGACG AAAATGGTGA
2451 CAAGACAGAT GGCCAGAAAT ACACCAACAG CACGCAATGAT GTCTACTGGG GATTTATTCT TTAGTGGGG
2521 GGAATACACG GCTTTTAATA CGATTGAGGG CGTCTCTAA CAAGTACAT CACTCCTGCC CTTCCCTCACC
2591 CTCATCTCCA TACACCTCTT CATCTCCGTC ATCTCCGTC TACACCTCTCG CGGCAGCCCC TTCCACCATATA
2661 GGTGGAAACCG AGGGAGGCAA ATCTACTCCA TCGTCAAAGC TGACACAGT CACCCGTATA TTGCAAGGTAG
2731 GAGCGGGCTT TGTCTATAACA AGGTCTCTAA TCGCATCTCTT CAAAACCTCA GCAAATAAT GAGTTGTAA
2801 AAAGACCATG AAATAACAGA CAATGGACTC CCTTGTAGGG CGCAGGTGTC GATTTATTCT TTAGTGGGG
2871 CCAAAGGGGA GACGACTCAA TGGTGTAAAGA CGACATTGTC GAATAGCAAG GGCAGTTCT CGCCTTAGGT
2941 TGTAAGGGGA GGTCTCTACTA CCTCCATATA CGAACACACC GGCACCCAA GTTCTCTCG CGGTAGCCT
3011 TTCTACGTGA CTCCCTAGCCA GGAGAGCTCT TAAACCTCTC GCAATGTCT CAAATTTGG GTTGAACCT
3081 CCTTGACAC GATGCTCTTCA AAACACCCCT CTTTGTGCT GCCTGCTCTTCTC ATCACCTGCA CCCCCGGGTG
3151 CAGTGCTGGG GCCTCTCTC GGTGCTATCG CGGGGCCCTG CTCTATCGT CCGGGGGCA CGTCAGGCTC
3221 ACCATCTGGG CCACCTCTCTT GGTGGTATTTC AAAATAATCG GCTTCTCTA CAGGGTGGAA AAATGGCCTT
3291 CTACCTGGAG GGGGCTGCG CGGTGGAGAC CGGGATGATG ATGACTGACT ACTGGGACTC CTGGGCTCT
3361 TTTCGCTACG TCCACGACCT CTCCCCCTGG CTCTCTCACG ACTTCCCCCC CTGGCTCTT CACGTCCT
3431 ACCCCGCGG CTCACACTA CTCCCTGACC CGGGCTCTCA TACACCTCTC GACCCGGGG TCCACTGCCT
3501 CCTCGACCCC GGGCTCCACC TCCTGCTCTT GCCCCCTCTG CTCCCTGCCCG TCCTCTCTGCT CCTGCCCTC
3571 CTGCCCTCTC TGCTCTGCTC CCTCTGCCCC CTCCCTGCTC TGCCCCCTCTC CTGCTCTCTGCT CCTCTGCC
3641 TCCTGCCCCCT CCTCTGCTC CTGCCCCCTCC TGCCCCCTCTC CCTGCTCTGCTC CCCTCTCTGCT
3711 CCTGCCCTCTC TGCCCCCTCTC TGCTCTGCCC CCTCTGCCCC CTCCCTGCTC TGCCCCCTCTC CCTCTGCTC
3781 CTCTGCTCTC TGCCCCCTCTC TGCTCTGCCC CCTCTGCCCC CCTCTGCCCC CTCCCTGCTC TGCCCCCTCTC
3851 TGCTCTGCTC CCTCTGCCCC TGCTCTGCTC TGCTCTGCTC TGCCCCCTCTC TGCTCTGCTC CCTCTCTGCT
3921 CCTCTGCCCC TGCTCTGCTC CCTCTGCCCC TGCTCTGCTC TGCCCCCTCTC CCTCTGCTC TGCCCCCTCTC
3991 CCCCCTCTGC CCTCTCTGCTC CCTCTCTGCTC TGCTCTGCCCC TGCTCTGCCCC TGCTCTGCTC TGCTCTGCCCC
4061 TCCCTGCTCTC CCTCTGCTCTC TGCCCCCTCTC CCTCTGCTCTC TGCTCTGCTC TGCTCTGCTC TGCTCTGCTC
4131 CCTGCCCTCTC TGCCCCCTCTC TGCCCCCTCTC CCTCTGCTCTG TGCTCTGCTC TGCTCTGCTC TGCTCTGCTC
4201 CTGCCCTCTC CGCTCTGCTC CCTCTGCTCTG TTCCACCGTG GGTCCCTTTG CAGCCAATGTC AACTTGAGC
4271 TTTTGGGGT CCTCGGACAC CATCTCTGAT TCTTGGCCCT GATCTGAGC CGCCCGGGGC TCCTGGTCTT
4341 CCGCCCTCTC GTCTCTGCTC TCTTCCCCGT CCTCGTCCAT GGTATCACC CCCTCTCTT TGAGGTCAC
4411 TGCGGCCGGA CCTCTGCTGGT CCAGATGTGT CTCCCTCTC TCTCTAGGCCA TTCCAGGTC CTGTACCTGG
4481 CCCCCTGCTCA GACATGATTC ACACAAAG AGATCAATAG ACATCTTTAT TAGACGACGC TCAGTGAATA
4551 CAGGGAGTGC AGACTCTGTC CCCCTCCAAAC AGCCCCCCCCA CCTCTCATCCC CTTCATGGTC GCTGTCAGAC
4621 AGATCCAGGT CTGAAAATTC CCCATCTCTC GAACCATCCT CGTCTCTCATC ACCAATTACT CGCAGCCCC
4691 AAAATCCCG CTGACATCC TCAAGATTG CGTCTGAGC CTCAAGGCCAG GCCTCAAATT CCTCGTCCCC
4761 CTTTTGCTG GACGGTAGGG ATGGGGATTG CGGGGACCCC TCCCTCTCTT CTTCAAGGTC ACCAGACAGA
4831 GATGCTACTG GGGCAACGGA AGAAAAGCTG GGTGCGGCCCT GTGAGGATCA GCTTATCGAT GATAAGCTG

4901 CAAACATGAC AATTCTTGA GACGAAAGGG CCTCGTATA CGCCTATT TATAGTTAA TGTATGATA
 4971 ATAATGGTTT CTTAGACGTC AGGTGGCACT TTTCGGGAA ATGTGCGCGG AACCCTATT TGTTTATT
 5041 TCTAAATACA TTCAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTCAAT AATATTGAAA
 5111 AAGGAAGAGT ATGAGTATTG AACATTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT TTGCCCTCCT
 5181 GTTTTGCTC ACCCAGAAC GCTGCTGAAA GTAAAGATG CTGAAGATCA GTGGGGTGC CGAGTGGTT
 5251 ACATCGAAT GGATCTCAAC ACGGTAAGA TCCTTGAGAG TTTTCGCCCCA GAAGAACGTT TTCAATGAT
 5321 GAGCACTTTT AAAGTCTG CTTAGTGGCGC GGTATTATCC CGTGTGACG CCGGGCAAGA GCAACTCGGT
 5391 CGCCGCATAC ACTATTCTCA GAATGACTG GTTGAGTACT CACCAAGTCAG AGAAAAGCAT CTTACGGATG
 5461 GCATGACAGT AAAGAGAATTA TGCACTGCTG CCATAACCAT GAGTGAATAC ACTGCGGCCA ACTTACTCT
 5531 GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT
 5601 GATCGTTGGG AACCGGAGCT GAATGAAGC ATACCAAAACG ACGAGCGTGA CACCAAGATG CCGCAGCAA
 5671 TGGCAACAAC GTTGCAGCAA CTATTAACG GCGAAGTACT TACTCTAGCT TCCCGGCAAC AATTAATAGA
 5741 CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTTATTGCT
 5811 GATAATCTG CGCCGGTGA CGCTGGCTC CGCGGTATCA TTGAGCAGACT GGGGCCAGAT GGTAAGCCCT
 5881 CCCGTATCGT AGTATCTAC ACGACGGGG TGCAAGCAAC TATGGATGAA CAAATAGAC AGATCGCTGA
 5951 GATAGGTGCC TCAGTGTGATTA AGCATTTGTA ACTGTCAGAC CAAGTTACT CATATATACT TTAGATTGAT
 6021 TAAAAACTTC ATTTTAATT TAAAAGGATC TAGGTGAGA TCCCTTTGTA TAATCTCATG ACCAAAATCC
 6091 CTTAACGTGA GTTTCTGTTT CACTGAGCGT CAGACCCCGT AGAAAAGATC AAAGGATCTT TTGAGATCC
 6161 TTTTTCTG CGCGTAACTCT GCTGCTTGC AAAAAAAA CCACCGCTCA CAGGGTGGG TTGTTTGC
 6231 GATCAAGAGC TACCAACTCT TTTTCCCGAG GTAACTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC
 6301 TTCTAGTGTG CCGTAGTTA GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT
 6371 AATCTGTGTA CCACTGGCTG CTGCGAGTGG CGATAAGTCC TGTCTTACCG GTTGGACTC AAGACGATAG
 6441 TTACCGGATC AGGCGACGGC GTCGGGCTGA ACGGGGGTT CGTGCACAC GCCCAGCTTG GAGCGAACGA
 6511 CCTACACCGA ACTGAGATAC CTACAGCTG AGTATGAGA AAGCAGCCACG CTTCCCGAAG GGAGAAAGC
 6581 GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC
 6651 TGGTATCTT ATAGTCTGTG CGGGTTTCCG CACCTCTGAC TTGAGCAGTCG ATTGGTGTGA TGCTCGTCAG
 6721 GGGGGCGAG CCTATGGAAA AACGCCAGCA ACGCGGCCCTT TTACGGTTT CCGGCTTTT GCTGCGCCGC
 6791 GTGCGGCTG TGAGGATGGC GGAGCGATG GATATGTTT GCGCAAGGGTT GTTTTGCAGCA TTACAGTT
 6861 CCTCGAAGAA TTGATTGGCT CCAATTCTG GAGTGGTGA TCCGTTAGCG AGGCCATCCA GCCTCGCGTC
 6931 GAACTAGATG ATCCCTGTG GAATGTGTT CAGTTAGGGT GTGAAAGTC CCCAGGCTCC CCAGCAGGCA
 7001 GAAAGTATGCA AACGATGCTC CTCAATTAGT CAGCAACACG GTGTTGAAAG TCCCCAGGCT CCCCAGCAGG
 7071 CAGAAGTATG CAAACATGCA ATCTCAATTAGT GTCAGCAACCG ATAGTCCCGC CCTCAACTCC GCCCCATCCG
 7141 CCCCTAACTC CGCCCACTTC CGCCCAATTCTT CCGCCCATG GCTGACTAAT TTTTTTATT TATGCAGAGG
 7211 CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG AGGAGGCTTT TTTGGAGGGT GACCGCCACG
 7281 ACCGGTGCAG CGACCATCCCG CTGACCCACG CCCCCTGACCC CTACAAGGA GACGACCTTC CATGACCGAG
 7351 TACAAGCCCA CGGTGCGCTC CGCCACCCCG GACGACGTC CCGGGCCCGT ACGACCCCTC GCGCCCGCGT
 7421 TCGCCGACTA CCCCCCGCACG CGCCACACCG TCGACCCCGA CCGCACACATC GAACCGCTCA CCGAGCTGCA
 7491 AGAACTCTTC CTCACGCGCG TCGGGCTCGA CATCGGCAAG GTGTTGGTCG CGGACGACGG CGCCGCGGTG
 7561 GCGGCTGGA CCACGCCGA GAGCGCTCGA GCGGGGGCG TGTTCGCGCA GATCGCCCG CGCATGGCCG
 7631 AGTTGAGCGG TTCCCGGCTG GCGCGCAGC AACAGATGGA AGGCTCTCTG GCGCCGCACC GGGCCAAGGA
 7701 GCGGGCTGG TTCCCTGGCCA CGGTGGCGT CTCGCCCCGAC CACCGGGCA AGGGTCTGG CAGCGCGTC
 7771 GTGCTCCCCG GAGTGGAGGC GGCGAGCGC GCGGGGGTGC CCGCTTCTC GGAGACCTCC GCGCCCCGCA
 7841 ACCTCCCTT CTACGAGCGG CTCGGCTCTCA CCGTCACCGC CGACGTCGAG TGCCGAAGG ACCGCGCGAC
 7911 CTGGTGCATG ACCCGCAAGC CCGGTGCTG ACGCCCGCCC CACGACCCCG AGCGCCCGAC CGAAAGGAGC
 7981 GCACGACCCG GTCCGACGGC GGCCACCCGG TCCCAAGGGG TGCGACCTCG AAACATTGTT ATTGCAGCTT
 8051 ATAATGGTTA CAAATAAACG AATAGCATCA CAAATTTCAC AAATAAAAGCA TTTTTTAC TGCATTCTAG
 8121 TTGTGGTTT TCCAAACTCA TCAATGTATC TTATCATGTC TGATCGATC CGAACCCCT CCTCGACCCAA
 8191 TTCTCATGTT TGACAGCTTA TCATCGAGA TCCGGGCAAC GTTGTGTCAT TGCTGAGGC GCAGAACTGG
 8261 TAGGTATGGA AGATCTATAC ATTGAATCAA TATTGGCAAT TAGCATATT AGTACATT ATTGTACATT ATATTGGCTC
 8331 AAATCAATAT TGGTATTG CATTGTCATA CGTTGTATCT ATATCATAAT ATGTACATT ATGTACATT
 8401 ATGTCCAATA TGACCGCCAT GTTGACATTG ATTATGACT AGTATTAAAT AGTAATCAAT TACGGGGTCA
 8471 TTAGTTCATC GCCCATATAT GGAGTTCGCG GTTACATAAC TTACGGTAAAG TGGCCCGCCT GGCTGACCGC
 8541 CCAAGACCC CGGGCCATTG ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCAATAG GGACTTCCA
 8611 TTGAGCTAA TGGGTGGAGT ATTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGT TAATATGCCA
 8681 AGTCGCCCC CTATTGACGT CAATGACGGT AAATGCCCG CCTGGCATTA TGCCCACTAC ATGACCTTAC
 8751 GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACG ATGGTGTATGC GGTTTGGCA
 8821 GTACACCAAT GGGCGTGGAT AGCGGTTGTA CTCACGGGGA TTTCAGGTC TCCACCCCAT TGACGTCAT
 8891 GGGAGTTGT TTTGGCACC AATACACCG GACTTTCAA AATGTCGTA TAACCCGCC CGTTGACGC
 8961 AAATGGCGG TAGGCGTGTG CGGTGGAGG TCTATATAAG CAGAGCTCGT TTAGTGAACCG GTCAGATCTC
 9031 TAGAAGCTGG GTACCGGGAT CCAGCAGCTG GGCTCGAGGT GCTACGGGAA GGGGGTGGAT GTGGGATCGA
 9101 AGGTGCGAAG CTTACTCACA CATGCCACCG TGCCCGCAGCA CCTGAAGCCG AGGGGGCACC GTCACTCTTC
 9171 CTCTTCCCCC CAAACACCCAA GGACACCCCT ATGATCTCCC GGACACCCCTGA GGTACATGCG TGTTGGTGG
 9241 ACGTGAGCCA CGAAGACCC GAGGTCAAGT TCAACTGGTA CGTGGACGCC GTGGAGGTGCA ATAATGCCAA
 9311 GACAAAGCCG CGGGAGGAGC AGTACACAG CACGTCACCGT GTGGTCAAGCG CCCTCACCGT CCTGCACCA
 9381 GACTGGTGA ATGGCAAGGA GTACAAGTGC AAGGTCTCCA ACAAAAGCCCT CCCAGCCTCC ATCGAGAAAAA
 9451 CCATCTCAA AGGCAAGGG CAGCCCGAG AACACACGGT GTACACCCCTG CCCCCCATCCC GGGATGAGCT
 9521 GACCAAGAAC CAGGTAGCC TGACCTGCC GGTCAAAGGC TTCTATCCCA GCGACATCGC CGTGGAGTGG
 9591 GAGAGCAATG GGCAGCCGG AACAACACTAC AAGACACCGC CTCCCGTGTG GGACTCCGAC GGCTCCCTCT
 9661 TCCTCTACAG CAAGCTCACCGT GTGGACAAGA CGAGGTGGCA GCAGGGGAAC GTCTTCTCAT GCTCCGTGAT
 9731 GCATGAGGCT CTGCACAAAC ACTACACCGA GAAGAGCCTC TCCCTGTCTC CGGGTAAATG ACTCGAGGCC
 9801 CGAACAAAAA CTCATCTAC AGAGGATCT GAATAGCGCC GTCGACCATC ATCATCATCA TCATTGAGTT
 9871 TNAACGATCC AGACATGATA AGATACATTG ATGAGTTGG ACAAAACCACA ACTAGAATGC AGTGAAGAAA
 9941 ATGCTTATT TGTGAAATTG TGATGCTAT TGTCTTATTG GTAACCCATTAA TAAGCTGCAA TAAACAAAGTT
 10011 AACAAACAAC AATGCAATTCA TTTTATGTTT CAGGTTCAAGG GGGAGGTGGG GAGGTTTTT AAAGCAAGTA
 10081 AACCTCTAC AAATGTGGTA TGGCTGATTA TGATCCGGCT GCCTCGCCG TTTGGTGT GACGGTGGAAA
 10151 ACCTCTGACA CATGCAGCTC CGGGAGACGG TCACAGCTTG TCTGTAAGCG GATGCCGGGA GCAGACAAGC
 10221 CGTCAGGGC CGCTCAGCGG GTGTTGGCGG GTCTCGGGGC GCAGGCGATCA CGGGTCGACT CTAGA

284:

5'LT• : (SEQ ID NO:284)

5'-CTT GGT GCC GCA GGA TCA G-3'

285:

3'LT• : (SEQ ID NO:285)

5'-CAG ATG GCT GTC ACC CCA C-3'

286:

5'LT• long-*NheI*: (SEQ ID NO:286)

5'-GCC CGC TAG CCT GCG GTG GTC AGG ATC AGG GAC GTC G-3'

287:

5'LT• short-*NheI*: (SEQ ID NO:287)

5'-GCC CGC TAG CCT GCG GTG GTT CTC CAG CTG CGG ATT C -3'

288:

3'LT• stop-*NotI*: (SEQ ID NO:288)

5'-CAA TGA CTG CGG CCG CTT ACC CCA CCA TCA CCG -3'

289:

GST-EK-C-LT• ₄₉₋₃₀₆: SEQ ID NO:289

APLVMSPLGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQ
SMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFDRLCH
KTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAPIQIDKYLKSSKYIAWPLQGWQATF
GGGDHPPKASMTGGQQMGRDLYDDDDKLACGGQDQGRRVEKIIGSGAQAQKRLDDSKPSCILPSPSSL
SETPDPRLHPQRSNASRNLASTSQGPVAQSSREASAWMTILSPAADSTPDPGVQQLPKGEPETDLNPEL
PAAHLIGAWMSGQGLSWEASQEEFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGRTPPAGRSRARS
LTLLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGYGSLWYTSVGFGLAQLRSGERVYVNISHPDMV
DYRRGKTFVGAVMVG

290:

GST-EK-C-LT• ₁₂₆₋₃₀₆: SEQ ID NO:290

APLVMSPILGWIKGLVQPTRLLEEKYEEHYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQ
SMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIYGVSRAYSQDFETLKVDFLSKLPEMLKMFEDRLCH
KTYLNGDHVTHPDFMLYDALDVLYMDPMCLDAFPKLVCFKKRIEAPIQIDKYLKSSKYIAWPLQGWQATF
GGGDHPPKASMTGGQQMGRDLYDDDDKLACGGSPAADSTPDGVQQLPKGEPETDLNPELPAAHLIGA
WMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGRTPPAGRSRARSLLRSALY
RAGGAYGRGSPELLEGAETVTPVVDPIGY GSLWYTSVFGGLAQLRSGERVYVNISHPDMVDYRRGKT
FFGAVMVG

291:

his-myc-EK-C-LT• 49-306: SEQ ID NO:291

APLVHHHHHGPLVDVASNEQKLISEEDLASMTGGQQMGRDLYDDDDKLACGGQDQGRRVEKIIGSGAQ
AQKRLDDSKPSCILPSLSETPDPRHPQRSNASRNLASTSQGPVAQSSREASAWMTSPAADSTPDGV
QQLPKGEPETDLNPELPAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGY
RGRTPPAGRSRARSLLRSALYRAGGAYGRGSPELLEGAETVTPVVDPIGY GSLWYTSVFGGLAQLRSGERVY
ERVYVNISHPDMVDYRRGKTFFGAVMVG

292:

his-myc-EK-C-LT• 126-306: SEQ ID NO:292

APLVHHHHHGPLVDVASNEQKLISEEDLASMTGGQQMGRDLYDDDDKLACGGSPAADSTPDGVQQLP
KGEPETDLNPELPAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGRT
PPAGRSRARSLLRSALYRAGGAYGRGSPELLEGAETVTPVVDPIGY GSLWYTSVFGGLAQLRSGERVY
VNISHPDMVDYRRGKTFFGAVMVG

293:

primerMCS-1F

5'-TAT GGA TCC GGC TAG CGC TCG AGG GTT TAA ACG GCG GCC GCA T-3' (SEQ ID NO:293)

294:

primerMCS-1R

5'-TCG AAT GCG GCC GCG GTT TAA ACC CTC GAG CGC TAG CCG GAT CCA-3' (SEQ ID NO:294)

295:

Bamhis6-EK-Nhe-F

5'-GAT CCA CAC CAC CAC CAC CAC GGT TCT GGT GAC GAC GAT GAC AAA GCG CTA GCC C-3'
(SEQ ID NO:295)

296:

Bamhis6-EK-Nhe-R

5'-TCG AGG GCT AGC GCT TTG TCA TCG TCG TCA CCA GAA CCG TGG TGG TGG TGG TGG TGT G-3'
(SEQ ID NO:296)

297:

oligo1F-C-glycine-linker

5'-TCG AGG GTG GTG GTG GTG GTT GCG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:297)

oligo1F-C-glycine-linker
oligo1R-C-glycine-linker
oligo1F-C-gamma1-linker
oligo1R-C-gamma1-linker
oligo1FA-C-gamma3-linker
oligo1RA-C-gamma3-linker

298:

oligo1R-C-glycine-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCG CAA CCA CCA CCA CCC-3' (SEQ ID NO:298)

299:

oligo1F-C-gamma1-linker

5'-TCG AGG ATA AAA CCC ACA CCT CTC CGC CGT GTG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:299)

300:

oligo1R-C-gamma1-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCA CAC GGC GGA GAG GTG TGG GTT TTA TCC-3' (SEQ ID NO:300)

301:

oligo1FA-C-gamma3-linker

5'-TCG AGC CGA AAC CGT CTA CCC CGC CGG GTT CTT CTG-3' (SEQ ID NO:301)

302:

oligo1RA-C-gamma3-linker

5'-CAC CAC CAG AAG AAC CCG GCG GGG TAG ACG GTT TCG GC-3' (SEQ ID NO:302)

303:

oligo2FB-C-gamma3-linker

5'-GTG GTG CTC CGG GTG GTT GCG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:303)

304:

oligo2RB-C-gamma3-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCG CAA CCA CCC GGA G-3' (SEQ ID NO:304)

305:

rMIF-F

5'-GGA ATT CCA TAT GCC TAT GTT CAT CGT GAA CAC-3' (SEQ ID NO:305)

306:

rMIF-Xho-R

5'-CCC GCT CGA GAG CGA AGG TGG AAC CGT TC-3' (SEQ ID NO:306)

307:

rMIF-C1:

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ
NRNYSKLLCGLLSDRLHISPDRVYINYDMNAANVGWNGSTFALEGGGGGCG (SEQ ID NO:307)

308:

rMIF-C2

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ
NRNYSKLLCGLLSDRLHISPDRVYINYDMNAANVGWNGSTFALEDKTHTSPPCG (SEQ ID NO:308)

309:

rMIF-C3

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ
NRNYSKLLCGLLSDRLHISPDRVYINYDMNAANVGWNGSTFALEPKPSTPPGSSGGAPGGCG (SEQ ID
NO:309)

310:

met-human-MIF-C1

MPMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFALEGGGGGCG

311:

human-MIF-C1 (SEQ ID NO:311)

PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFALEGGGGGCG

312:

met-human-MIF-C2 (SEQ ID NO:312)

MPMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFALEDKHTSPPCG

313:

human-MIF-C2 (SEQ ID NO:313)

PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFALEDKHTSPPCG

314:

met-human-MIF-C3 (SEQ ID NO:314)

MPMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFALEPKPSTPPGSSGGAPGGCG

315:

human-MIF-C3 (SEQ ID NO:315)

PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFALEPKPSTPPGSSGGAPGGCG

316:

RANKL-UP:

5'CTGCCAGGGGCCGGTGC GGCGGTGCCATCATCACCA CACCAGCGCTTCTCAGGAG-3'

317:

RANKL-DOWN :

5'-CCGCTCGAGTTAGTCTATGTCCTGAACTTGAAAG-3'

318 and 319:

Protein sequence of GST-PS-C-RANKL (SEQ ID NO:318; capital letters)

cDNA sequence of GST-PS-C-RANKL (SEQ ID NO:319; small letters)

1 M S P I L G Y W K I K G L V Q P T R L L L E Y L E
1 atgtccctatacttaggttattggaaaattaaggccctgtcaacccactcgacttctttggaatatctgaa
26 E K Y E E H L Y E R D E G D K W R N K K F E L G L
76 gaaaaatataaagagcattgttatgagcgcgatgaaggtataatggcggaaaaaagttgaattgggttg
51 E F P N L P Y Y I D G D V K L T Q S M A I I R Y I
151 gagttcccaatcttattatattatgtatggatgtttaaataacacatgttgcattatacgttatata
76 A D K H N M L G G C P K E R A E I S M L E G A V L
226 gctgacaaggacaacatgttgggtgttgcggaaaagagcgtgcagagatttcaatgttgcaggagcgggtttg
101 D I R Y G V S R I A Y S K D F E T L K V D F L S K
301 gatattagatacggttgcgatgttgcataatagaagactttggaaactctaaatggatgttttttagcaag
126 L P E M L K M F E D R L C H K T Y L N G D H V T H
376 ctacctgaaatgtcggaaaatgttgcgatgttgcataaaaacatattttaaatggatgttgcattataccat
151 P D F M L Y D A L D V V L Y M D P M C L D A F P K
451 cctgacttcatgttgcgatgttgcggccatgttgcctggatgcgttttttttttttttttttttttttttttt
176 L V C F K K R I E A I P Q I D K Y L K S S K Y I A
526 ttagttgttt
201 W P L Q G W Q A T F G G G D H P P K S D L E V L F
601 tggcccttgcggggccatgttgcggccacgttgcggccatgttgcggccatgttgcggccatgttgcggcc
226 Q G P G C G G G H H H H Q R F S G A P A M M E
676 caggGGGCCGGGTGCGCGGGCCATCATCACACCACATCACAGCGCTCTCAGGAGCTCCAGCTATGATGGAA
251 G S W L D V A Q R G K P E A Q P F A H L T I N A A
751 GGCTCATGGTGTGGATGTGGCCCAGCGAGGCAAGGCCGTAGGCCAGCCATTGACACCTCACCATCAATGCTGCC
276 S T P S G S H K V T L S W Y H D R G W A K T I S N
826 AGCATCCCATCGGGTTCATCAAAGTCACTCTGCTCTTGGTACCGATCGAGGCTGGGCCAAGATCTCAAC
301 M T L S N G K L R V N Q D G F Y Y L Y A N I C F R
901 ATGACGTTAACGAAACGAAACTAACGGTTAACCAAGATGGCTTATTACCTGTACGCCAACATTGCTTTCGG
326 H H E T S G S V P T D Y L Q L M V Y V V K T S I K
976 CATCATGAAACATCGGGAAAGCGTACACTACAGACTATCTCAGCTGATGGTGTATGCTTAAACCCAGCATCAAA
351 I P S S H N L M K G G S T K N W S G N S E F H F Y
1051 ATCCCAAGTTCTCATAACCTGATGAAAGGGAGGAGCAGAAAAACTGGTGGGCAATTCTGAATTCCACTTTAT
376 S I N V G G F K R L R A G E E I S T Q V S N P S L
1126 TCCATAATGTTGGGGATTTCAAGCTCGAGCTGGTGAAGAAATTAGCATTCAGGTGTCCAACCCCTCCCTG
401 L D P D Q D A T Y F G A F K V Q D I D *
1201 CTGGATCCGGATCAAGATGCGACGTACTTGGGGCTTCAAAGTTCAAGGACATAGACTAACCTCGAGCGG

320:

Human-C-RANKL

CGGGQHIRAEKAMVDGSWLDLAKRSKLEAQPFKAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLI
VNQDGFYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGSTKYWSGNSEFHYSINVGGFFK
LRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID

321:

Primer 5'PrP-BamHI

5'-CGG GAT CCC ACC ATG GTG GGG GGC CTT GG -3' (SEQ ID NO:321)

322:

Primer 3'PrP-NheI

5'-CTA GCT AGC CTG GAT CTT CTC CCG -3' (SEQ ID NO:322)

323:

Protein sequence of mPrP_t-EK-Fc*

MVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYPVDQYSNQNNFVHDCVNITIKQHT
VTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRSRLAGGGCGDDDDKLTHTCPPCPAPEA
EGAPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
K

324:

mPrP_t

MVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYPVDQYSNQNNFVHDCVNITIKQHT
VTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRSRLAGGGCGDDDDK

325:

human resistin-C-Xa: (SEQ ID NO:325)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDL
ATCPRGFATGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG
IEGR

326:

human resistin-C-EK: (SEQ ID NO:326)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDL
ATCPRGFATGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG
DDDK

327:

human resistin-C: (SEQ ID NO:327)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDL
ATCPRGFATGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG

328:

mouse C-IL-13-F: (SEQ ID NO:328)

ADPGCGGGGLAGPVPRSVSLPLTLKELIEELSNITQDQTPLCNGSMVWSVDAAGGFCVALDSLTNISNCN
AIYRTQRILHGLCNRKAPTTVSSLPDTKIEVAHFITKLLSYTKQLFRHGPFLEVLAIEGR
329:

mouse C-IL-13-S: (SEQ ID NO:329)

LACGGGGGPVPRSVSLPLTLKELIEELSNITQDQTPLCNGSMVWSVDAAGGFCVALDSLTNISNCNAI
YRTQRILHGLCNRKAPTTVSSLPDTKIEVAHFITKLLSYTKQLFRHGPF

330:

human C-IL-13-F: (SEQ ID NO:330)

ADPGCGGGGLAGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCS
AIEKTQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKKLFREGRFNLEVLAIEGR

331:

human C-IL-13-S: (SEQ ID NO:331)

LACGGGGGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQR
MLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKKLFREGRFN

332:

mouse C-IL-5-E: (SEQ ID NO:332)

ALVGCGGPKPSTPPGSSGGAPASMEIPMSTVVKETLTQLSAHALLTSNETMRLPVPTHKNHQLCIGEIFQG
LDILKNQTVRGGTVEMLFQNLNSLIKYYIDRQKEKCIGEERRTRQFLDYLQEFLGVMSTEWAMEG

333:

mouse C-IL-5-F: (SEQ ID NO:333)

ADPGCGGGGLAMEIPMSTVVKETLTQLSAHALLTSNETMRLPVPTHKNHQLCIGEIFQGLDILKNQTVR
GGTVEMLFQNLNSLIKYYIDRQKEKCIGEERRTRQFLDYLQEFLGVMSTEWAMEGLEVLAIEGR

334:

mouse C-IL-5-S: (SEQ ID NO:334)

LACGGGGGMEIPMSTVVKETLTQLSAHALLTSNETMRLPVPTHKNHQLCIGEIFQGLDILKNQTVRG
TVEMLFQNLNSLIKYYIDRQKEKCIGEERRTRQFLDYLQEFLGVMSTEWAMEG

335:

human C-IL-5-E: (SEQ ID NO:335)

ALVGCGGPKPSTPPGSSGGAPASIPTEIPTSAVKETLALLSTHRTLLIANETLRIPVPHKNHQLCTEEIFQGI
GTLESQTVQGGTVERLFKNLNSLIKYYIDGQKKCIGEERRRVNQFLDYLQEFLGVMNTIEWIIES

336:

human C-IL-5-F: (SEQ ID NO:336)

ADPGCGGGGLAIPTEIPSTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQG
GTVERLFKNLSLIKYYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEW IIES LEVLAIEGR

337:

human C-IL-5-S: (SEQ ID NO:337)

LACGGGGIPTEIPSTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGGT
VERLFKNLSLIKYYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEW IIES

338:

primer NheIL13-F: (SEQ ID NO:338)

CTAGCTAGCCGGGCCGGTGCCAAGATC

339:

primer XhoIL13-R: (SEQ ID NO:339)

TTTCTCGAGGAAGGGGCCGTGGCGAA

340:

primer Spelinker3-F1: (SEQ ID NO:340)

CCCCGCCGGTTCTCTGGCGGTGCTCCGGCTAGCATGGAGATTCCCATGAGCAC

341:

Primer SpeNlinker3-F2: (SEQ ID NO:341)

TTTTACTAGTTGGTTGCGGCCGCCGAAACCGAGCACCCCGCCGGTTCTTC

342:

Primer IL5StopXho-R: (SEQ ID NO:342)

TTTGCGGCCGCGTTAAACTCGAGTTATTAGCCTTCCATTGCCCACTC

343:

Primer BamH1-FLK1-F: (SEQ ID NO:343)

CGCGGATCCATTCATGCCCTCTGTC

344:

Primer Nhe1-FLK1-B: (SEQ ID NO:344)

CTAGCTAGCTTGTGTGAACCTGGAC

345:

mVEGFR-2 (2-3) fragment: (SEQ ID NO:345)

PFIAS VSDQHGIVYI TENKNKTVVI PCRGSISNLN VSLCARYPEK RFVPDGNRIS WDSEIGFTLP
SYMISYAGMV FCEAKINDET YQSIMYIVVV VGYRIYDVIL SPPHEIELSA GEKLVLNCTA
RTELNVGLDF TWHSSPSKSH HKKIVNRDVK PFPGTVAKMF LSTLTIESVT KSDQGEYTCV
ASSGRMIKRN RTFVRVHTKP

346

human C-LT[•] 49-306 : (SEQ ID NO:346)

LACGGQDQGRRVEKIIGSGAQAKRLDDSKPSCILPSPSSLSETPDPRLHPQRSNASRNLASTSQGPVAQSSR
EASAWMTILSPAADSTPDPGVQQLPKGEPETDLNPELPAAHЛИGAWMSGQGLSWEASQEEAFLRSGAQFSP
THGLALPQDGVYLYCHVGYRGRTPPAGRSRARSLLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIG
Y GSLWYTSVGFGLAQLRSGERVYVNISHPDMVDYRRGKTFFGAVMVG

347

human C-LT[•] 126-306 : (SEQ ID NO:347)

LACGGSPAADSTPDPGVQQLPKGEPETDLNPELPAAHЛИGAWMSGQGLSWEASQEEAFLRSGAQFSP
THGLALPQDGVYLYCHVGYRGRTPPAGRSRARSLLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIG
Y WYTSVGFGLAQLRSGERVYVNISHPDMVDYRRGKTFFGAVMVG

348

Modified human prion protein fragment: (SEQ ID NO:348)

VGGLGGYMLGSAMSRPIIHFGSDYEDRYYRENMRYPNQVYYRPMDE
YSNQNNFVHDCVNITIKQHTVTTTKGENFTETDVKMMERVVEQMCITQYERESQAYYQ
RGRLAGGGCG

349

Modified bovine prion protein fragment: (SEQ ID NO:349)

VGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMRYPNQVYYRPMDE
YSNQNNFVHDCVNITVKEHTVTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQ
RGRLAGGGCG

350

Modified sheep prion protein fragment: (SEQ ID NO:350)

VGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDR
YSNQNNFVHDCVNITVKQHTVTTTKGENFTETDIKIMERVVEQMCITQYQRESQAYYQ
RGRLAGGGCG